

result No.	Query			Description		
	Score	Match	Length	DB	ID	
1	644	100.0	119	21	AAB34728	Human secreted pro
2	644	100.0	119	21	AAV82453	Human TGC-440 ser
3	644	100.0	119	21	AAV87317	Human signal pepti
4	644	100.0	119	21	AAV56668	Membrane-bound pro
5	644	100.0	119	22	AAU29093	Human PRO polypept
6	644	100.0	119	22	AAG53977	Amino acid sequenc
7	644	100.0	119	22	AAB87536	Human PROB42. Hom
8	644	100.0	119	22	AAB65191	Human PROB42. UNQ4
9	644	100.0	119	23	ABP54931	Human cytokine pro

(ALPH-) ALPHAGENE INC.

Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;

WPI: 2000-638211/61.

N-PSDB; AAC59829.

Novel proteins and polypeptides useful for the treatment of e.g. multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, cancer, Alzheimer's disease, Parkinson's disease, stroke, anemia and ulcers

Claim 92; Page 441-442; 493pp; English.

This invention relates to 59 human secreted proteins and the nucleotide sequences encoding them. Sequences AAC59788-C59846 and AAB34687-B34745 represent the proteins and their encoding nucleotide sequences, and sequences AAB34746-B34771 represent fragments of the proteins. Probes for the DNA sequences are represented by sequences AAC59847-C59596. The proteins exhibit neuroprotective, dermatological, immunosuppressive, antiinflammatory, antianemic, nootropic, dermatological, immunosuppressive, cerebroprotective, haemostatic, vulnery, cytoprotective, antipsoriatic, antibacterial, virucide, and fungicide activity. The proteins and nucleotide sequences are useful as nutritional sources or supplements and in research. The proteins are useful for treating immune deficiency and disorders, which may be genetic or resulting from infections, autoimmune disorders such as multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, and for treating myeloid or lymphoid cell deficiencies such as anaemias by regulating haematopoiesis. The proteins are also useful in compositions for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, for wound healing, tissue repair and replacement and in the treatment of wounds, incisions and ulcers. Other uses include in the treatment of central and peripheral nervous system and neuropathies such as Alzheimer's and Parkinson's diseases and Shy-Drager syndrome, and mechanical and traumatic disorders, such as spinal cord disorders, head trauma and stroke. The proteins may also be used as a contraceptive, and for treating coagulation disorders such as haemophilias. The protein and nucleotide sequences with cadherin activity are useful for treating cancer. Other uses for the protein include for inhibiting the growth, infection or function of, or killing, infectious agents such as bacteria, virus, fungi and other parasites, for effecting bodily characteristics such as height, weight, hair colour, effecting biorhythms or cardiac cycles or rhythms, effecting metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors, effecting behavioural characteristics, providing analgesic effects and for treating hyperproliferative disorders such as psoriasis.

Sequence 119 AA;

Query Match 100.0%; Score 644; DB 21; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.8e-66;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGQCECKDWFRLAP 60
|||||
1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGQCECKDWFRLAP 60

61 RRRKMTVSGLPKQPCDHFKNVKKTRHORHHRKPNKHSRACQQLKOCQLRSFALPL 119
|||||
61 RRRKMTVSGLPKQPCDHFKNVKKTRHORHHRKPNKHSRACQQLKOCQLRSFALPL 119

RESULT 2

AY82453

AY82453 standard; Protein; 119 AA.

AY82453;

30-JUN-2000 (first entry)

Human TGC-440 secretory protein SEQ ID NO:1.

XX TGC-440; secretory protein; immunological disease; infectious disease;
KW pulmonary function disorder; hepatic function disorder; nephrotropic;
KW gastrointestinal function disorder; antiinflammatory; immunomodulatory;
KW virucide; hepatotropic; antiasthmatic; antibacterial; vaccine;
KW hepatitis; nephritis; influenza; asthma; pulmonary hypertension;
KW pneumonia; Helicobacter pylori infection.

OS Homo sapiens.

XX WO200014226-A1.

XX 16-MAR-2000.

XX 02-SEP-1999; 99WO-JP04765.

XX 03-SEP-1998; 98JP-0250108.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Itoh Y, Ogi K, Tanaka H, Kitada C;

XX WPI: 2000-256978/22.

XX N-PSDB; AAA08343, AAA08344.

Secretory protein TGC440, antibodies to it and compounds promoting or inhibiting its activity for diagnosis and treatment of diseases of the immune system, lung, kidney, liver and intestinal system

Claim 1; Fig 1; 86pp; Japanese.

The present sequence represents a human secretory protein designated TGC-440. TGC-440 has antiinflammatory, nephrotropic, immunomodulatory, virucide, hepatotropic, antiasthmatic and antibacterial activities, and can be used in vaccines. TGC-440 and the polynucleotide sequence encoding it can be used to treat, prevent and diagnose immunological, lung, liver, kidney or gastrointestinal disorders and infectious diseases, such as hepatitis, nephritis, influenza, asthma, pneumonia, pulmonary hypertension, and Helicobacter pylori infection. An antibody immunospecific for TGC-440 is also useful in the above treatment and diagnosis, and also for quantifying the amount of TGC-440 in a liquid specimen.

XX Sequence 119 AA;

Query Match 100.0%; Score 644; DB 21; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.8e-66;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGQCECKDWFRLAP 60

DB 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGQCECKDWFRLAP 60

QY 61 RRRKMTVSGLPKQPCDHFKNVKKTRHORHHRKPNKHSRACQQLKOCQLRSFALPL 119

DB 61 RRRKMTVSGLPKQPCDHFKNVKKTRHORHHRKPNKHSRACQQLKOCQLRSFALPL 119

RESULT 3

RAY87317

ID AAY87317 standard; Protein; 119 AA.

XX AAY87317;

XX 11-MAY-2000 (first entry)

DE Human signal peptide containing protein HSPP-94 SEQ ID NO:94.

DE Human; signal peptide-containing protein; HSPP; diagnosis; cancer;

KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;

KW antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic;

KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;

KW reproductive disorder; developmental disorder; arteriosclerosis;

cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
Parkinson's disease; Huntington's diseases; ovulatory defect;
muscular dystrophy.

Homo sapiens.

WO200000610-A2.

06-JAN-2000.

25-JUN-1999; 99WO-US14484.

26-JUN-1998; 98US-0090762.

31-JUL-1998; 98US-0094983.

01-OCT-1998; 98US-0102886.

11-DEC-1998; 98US-0112129.

(INCY-) INCYTE PHARM INC.

Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
Akerblom IE, Au-young J, Yue H, Patterson C, Reddy R, Hillman JL;
Bandman O;

WPI: 2000-160673/14.
N-FSDB; AAZ98202.

New human signal peptide-containing proteins useful in treatment,
prevention and diagnosis of e.g. cancer, inflammation and
cardiovascular disease

Claim 1; Page 220-221; 327pp; English.

AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the
human signal peptide-containing proteins HSPp-1 to HSPp-134. HSPps have
anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic,
neuroprotective, cardiovascular and antiasthmatic activities, and can
be used in gene therapy. HSPps can be used to treat or prevent disorders
associated with decreased activity or function of HSPp. Antagonists of
HSPp are used to treat or prevent disorders associated with increased
activity or function of HSPp. Such diseases include cell proliferation
(including cancer), inflammation, cardiovascular, neurological,
reproductive or developmental disorders, (e.g. arteriosclerosis,
cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
asthma, Crohn's disease, microbial or other infections, congestive or
ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPp
nucleic acids can be used for the recombinant production of HSPp, for
detecting HSPp in standard hybridisation and amplification assays (for
diagnosis and monitoring), in gene therapy, as antisense,
triplex-forming or ribozyme therapeutics, for detecting related sequences
or genetic variations, and for chromosomal mapping. HSPp are also used to
raise specific antibodies (Ab) and to screen for agonists and
antagonists (potential therapeutic agents). Ab are used to diagnose, or
monitor, HSPp-related diseases (in usual immunoassays) as therapeutic
antagonists, in competitive drug screens, and for purification of HSPp
from natural sources.

Sequence 119 AA:

Query Watch 100.0%; Score 644; DB 21; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.8e-66;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 MKVLISLLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGQCECKDWFRLAP 60

D 1 MKVLISLLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGQCECKDWFRLAP 60

Y 61 RRFKFTVSLPKKQPCDHFHKGKGNKTKTHQRHHRKPNKHSRACQOFLKQCLRSFALPL 119

D 61 RRFKFTVSLPKKQPCDHFHKGKGNKTKTHQRHHRKPNKHSRACQOFLKQCLRSFALPL 119

RESULT 4

AAV66668

ID AAV66668 standard; protein; 119 AA.

XX AC AAV66668;

XX AC AAV66668;

XX DT 05-APR-2000 (first entry)

XX DE Membrane-bound protein PRO842.

XX DE Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;

XX DE pharmaceutical; receptor immunoadhesin; gene mapping.

XX KW Homo sapiens.

XX OS WO9963088-A2.

XX PN 09-DEC-1999.

XX PD 02-JUN-1999; 99WO-US12252.

XX PR 02-JUN-1998; 98US-0087607.

XX PR 02-JUN-1998; 98US-0087609.

XX PR 02-JUN-1998; 98US-0087759.

XX PR 03-JUN-1998; 98US-0087827.

XX PR 04-JUN-1998; 98US-0088021.

XX PR 04-JUN-1998; 98US-0088025.

XX PR 04-JUN-1998; 98US-0088028.

XX PR 04-JUN-1998; 98US-0088029.

XX PR 04-JUN-1998; 98US-0088030.

XX PR 04-JUN-1998; 98US-0088033.

XX PR 04-JUN-1998; 98US-0088326.

XX PR 05-JUN-1998; 98US-0088167.

XX PR 05-JUN-1998; 98US-0088202.

XX PR 05-JUN-1998; 98US-0088212.

XX PR 05-JUN-1998; 98US-0088217.

XX PR 09-JUN-1998; 98US-0088655.

XX PR 10-JUN-1998; 98US-0088722.

XX PR 10-JUN-1998; 98US-0088730.

XX PR 10-JUN-1998; 98US-0088734.

XX PR 10-JUN-1998; 98US-0088738.

XX PR 10-JUN-1998; 98US-0088740.

XX PR 10-JUN-1998; 98US-0088741.

XX PR 10-JUN-1998; 98US-0088742.

XX PR 10-JUN-1998; 98US-0088810.

XX PR 10-JUN-1998; 98US-0088811.

XX PR 10-JUN-1998; 98US-0088825.

XX PR 10-JUN-1998; 98US-0088826.

XX PR 11-JUN-1998; 98US-0088858.

XX PR 11-JUN-1998; 98US-0088861.

XX PR 11-JUN-1998; 98US-0088863.

XX PR 11-JUN-1998; 98US-0088876.

XX PR 12-JUN-1998; 98US-0089090.

XX PR 12-JUN-1998; 98US-0089105.

XX PR 16-JUN-1998; 98US-0089440.

XX PR 16-JUN-1998; 98US-0089512.

XX PR 16-JUN-1998; 98US-0089514.

XX PR 17-JUN-1998; 98US-0089532.

XX PR 17-JUN-1998; 98US-0089538.

XX PR 17-JUN-1998; 98US-0089598.

XX PR 17-JUN-1998; 98US-0089599.

XX PR 17-JUN-1998; 98US-0089600.

XX PR 17-JUN-1998; 98US-0089653.

XX PR 18-JUN-1998; 98US-0089801.

XX PR 18-JUN-1998; 98US-0089907.

XX PR 18-JUN-1998; 98US-0089908.

XX PR 19-JUN-1998; 98US-0089947.

XX PR 19-JUN-1998; 98US-0089948.

XX PR 19-JUN-1998; 98US-0089952.

XX PR 22-JUN-1998; 98US-0090246.

XX PR 22-JUN-1998; 98US-0090252.

XX PR 22-JUN-1998; 98US-0090254.

23-JUN-1998; 98US-0090349.
 23-JUN-1998; 98US-0090355.
 24-JUN-1998; 98US-0090429.
 24-JUN-1998; 98US-0090431.
 24-JUN-1998; 98US-0090435.
 24-JUN-1998; 98US-0090444.
 24-JUN-1998; 98US-0090445.
 24-JUN-1998; 98US-0090461.
 24-JUN-1998; 98US-0090472.
 24-JUN-1998; 98US-0090535.
 24-JUN-1998; 98US-0090538.
 24-JUN-1998; 98US-0090540.
 24-JUN-1998; 98US-0090557.
 25-JUN-1998; 98US-0090676.
 25-JUN-1998; 98US-0090678.
 25-JUN-1998; 98US-0090688.
 25-JUN-1998; 98US-0090690.
 25-JUN-1998; 98US-0090691.
 25-JUN-1998; 98US-0090694.
 25-JUN-1998; 98US-0090695.
 25-JUN-1998; 98US-0090696.
 26-JUN-1998; 98US-0090862.
 26-JUN-1998; 98US-0090863.
 01-JUL-1998; 98US-0091358.
 01-JUL-1998; 98US-0091360.
 01-JUL-1998; 98US-0091344.
 02-JUL-1998; 98US-0091478.
 02-JUL-1998; 98US-0091486.
 02-JUL-1998; 98US-0091519.
 02-JUL-1998; 98US-0091628.
 02-JUL-1998; 98US-0091628.
 02-JUL-1998; 98US-0091633.
 02-JUL-1998; 98US-0091646.
 02-JUL-1998; 98US-0091673.
 07-JUL-1998; 98US-0091978.
 07-JUL-1998; 98US-0091982.
 07-JUL-1998; 98US-0092182.
 10-JUL-1998; 98US-0092472.
 20-JUL-1998; 98US-0093339.
 30-JUL-1998; 98US-0094651.
 04-AUG-1998; 98US-0095282.
 04-AUG-1998; 98US-0095285.
 04-AUG-1998; 98US-0095301.
 04-AUG-1998; 98US-0095302.
 04-AUG-1998; 98US-0095318.
 04-AUG-1998; 98US-0095321.
 04-AUG-1998; 98US-0095325.
 10-AUG-1998; 98US-0095916.
 10-AUG-1998; 98US-0095929.
 10-AUG-1998; 98US-0096012.
 11-AUG-1998; 98US-0096143.
 11-AUG-1998; 98US-0096146.
 12-AUG-1998; 98US-0096329.
 17-AUG-1998; 98US-0096757.
 17-AUG-1998; 98US-0096766.
 17-AUG-1998; 98US-0096768.
 17-AUG-1998; 98US-0096773.
 17-AUG-1998; 98US-0096791.
 17-AUG-1998; 98US-0096867.
 17-AUG-1998; 98US-0096891.
 17-AUG-1998; 98US-0096894.
 17-AUG-1998; 98US-0096895.
 17-AUG-1998; 98US-0096897.
 18-AUG-1998; 98US-0096949.
 18-AUG-1998; 98US-0096950.
 18-AUG-1998; 98US-0096959.
 18-AUG-1998; 98US-0096960.
 18-AUG-1998; 98US-0097022.
 19-AUG-1998; 98US-0097141.
 20-AUG-1998; 98US-0097218.
 24-AUG-1998; 98US-0097661.
 26-AUG-1998; 98US-0097951.
 26-AUG-1998; 98US-0097952.

26-AUG-1998; 98US-0097954.
 26-AUG-1998; 98US-0097955.
 26-AUG-1998; 98US-0097971.
 26-AUG-1998; 98US-0097974.
 26-AUG-1998; 98US-0097978.
 26-AUG-1998; 98US-0097979.
 26-AUG-1998; 98US-0097985.
 26-AUG-1998; 98US-0098014.
 31-AUG-1998; 98US-0098525.
 16-SEP-1998; 98US-0100634.
 12-JAN-1999; 98US-0115565.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
 PI Wood WI, Yuan J;
 XX
 XX WPI; 2000-072883/06.
 DR N-PSDB; AA265001.
 XX
 PT Membrane-bound proteins and related nucleotide sequences
 XX
 PS claim 12; Fig 99; 822pp; English.
 XX
 CC The invention provides membrane-bound PRO polypeptides and
 CC polynucleotides encoding them. The PRO sequences of the invention were
 CC identified based on extracellular domain homology screening. The PRO
 CC sequences have homology with proteins including LDL receptors, TIE
 CC ligands and various enzymes. The membrane-bound proteins and receptor
 CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
 CC immunoadhesins, for instance, can be used as therapeutic agents to block
 CC receptor-ligand interactions. The membrane-bound proteins can also be
 CC employed for screening of potential peptide or small molecule inhibitors
 CC of the relevant receptor/ligand interaction. The PRO encoding sequences
 CC are useful as hybridization probes, in chromosome and gene mapping and in
 CC the generation of antisense RNA and DNA. PRO nucleic acid sequences
 CC will also be useful for the preparation of PRO polypeptides, especially
 CC by recombinant techniques.
 CC
 SQ Sequence 119 AA;
 Query Match 100.0%; Score 644; DB 21; Length 119;
 Best Local Similarity 100.0%; Pred. NO. 1.8e-66;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRRDQASRRWLQGGQCECKDWFLRAP 60
 DB 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRRDQASRRWLQGGQCECKDWFLRAP 60
 QY 61 RRKFTVSGLPKQKPCDHFPGKGNVKKTRHQHRRKPNKHSRACQOFLKQCQLRSFALPL 119
 DB 61 RRKFTVSGLPKQKPCDHFPGKGNVKKTRHQHRRKPNKHSRACQOFLKQCQLRSFALPL 119
 RESULT 5
 AAU29093
 ID AAU29093 standard; Protein; 119 AA.
 XX
 AC AAU29093;
 XX
 XT 18-DEC-2001 (first entry)
 XX
 DE Human PRO polypeptide sequence #70.
 XX
 KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
 KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
 KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WC200168848-A2.
 XX

can be used for genetic analysis of individuals with genetic disorders.

AA	Sequence	119 AA;
SO		

Query Match 100.0%; Score 644; DB 22; Length 119;

QV 1 MKVLISSLLLLPLMLMSMVSSSLNPGVARGHRDRGQASRRWLQEGGQCECKDWF LRA P 60

db
1 MKVLISSLLLLPLMLSMVSSSLNPGVARGHRDRGQASRRWLQEGGQCECKDWFRLAP 60

QY 61 RRKFMTVSGLPKKQCPCDHFKGNVKTRHQRHHRKPNKHSRACQQLKQCQLRSFALPL 119

61 RRKFMTVSGLPKKQPCDHFKGNVKTRHQRRHRKPNKHSRACQQFLKQCQLRSFALPL 119

RESULT 6

AAG63977
 ID AAG63977 standard: Protein: 119 AA.

XX
AC
AAG63977:

13-NOV-2001 (first entry)

XX
DE amino acid sequence of a human Inq104 polypeptide.

XX Human: lung cancer specific gene: LSG: Lng104: lung cancer.

[illegible]XX
PW
W0300161055-A2XX
22
CC-8750-2001[illegible]XX
12 555-2000-200075-0103199

XX

XX

XX 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1

DR N-PSDB; AAH77949, AAH77951.

PT New lung cancer specific gene for the treatment and diagnosis of lung

PT cancer -

Claim 2; Page 115-116; 119pp; English.

XX
CC
The exact sequence is encoded by a human lung cancer specific gene

CC (LSG), and represents a polypeptide designated Eng104. LSGs are useful
CC in the treatment and diagnosis of lung cancer. The treatment of lung
CC cancer comprises the administration of a molecule which down regulates
CC the expression of the gene encoding the LSG.

CC target cell expressing an LSG. Identification of potential therapeutic

CC screening molecules for an ability to bind to or decrease expression
CC of an LSG relative to LSG in the absence of the agent where the ability
CC of a molecule to bind to the LSG or decrease expression of the LSG is
CC indicative of the molecule being useful in imaging and treating lung
CC cancer.

Sequence 119 AA;

```
Query Match      100.0%; Score 644; DB 22; Length 119;
```

1 MWM TGGTITITIMMSWVSSINPGVARGHRDRGOASRRWLQEGGQCECKDWFLRAP 60

Qy
I MKVLISSLLPLMLMSVSSSLNPGVARGHRDRGQASKKWDEVEGGQCECECKDWIENH

1 MKVLTSSLTLLTPI.MTMSMVSSSLNPGVARGHBRDRGOASRRWLQEGGQCECKDWFRLAP 60

61 RRKFTVSLPKKQPCDHFKNVKKTRHQRHHRKPNKHSRACQFLKQCQLRSFALPL 119
|||||
61 RRKFTVSLPKKQPCDHFKNVKKTRHQRHHRKPNKHSRACQFLKQCQLRSFALPL 119
|||||

SUIT 7
B87538
AAB87538 standard; Protein; 119 AA.
AAB87538;

15-MAY-2001 (first entry)
Human PRO842.

Human; PRO protein; mapping.
Homo sapiens.

WO200116318-A2.
08-MAR-2001.

24-AUG-2000; 2000WO-US23328.
01-SEP-1999; 99WO-US20111.
15-SEP-1999; 99WO-US21090.

07-DEC-1999; 99US-0169495.
09-DEC-1999; 99US-0170462.
11-JAN-2000; 2000US-0175481.
18-FEB-2000; 2000WO-US04341.
18-FEB-2000; 2000WO-US04342.
22-FEB-2000; 2000WO-US04414.
01-MAR-2000; 2000WO-US05601.
03-MAR-2000; 2000US-0187202.
25-APR-2000; 2000US-0199397.
22-MAY-2000; 2000WO-US14042.
05-JUN-2000; 2000US-0209832.

(GETH) GENENTECH INC.

Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
WPI: 2001-183260/18.
N-PSDB; AAF92070.

Eighty four nucleic acids encoding PRO polypeptides, useful in
molecular biology, including use as hybridization probes, and in
chromosome and gene mapping.

Claim 12; Fig 26; 278pp; English.

The present sequence is a human PRO polypeptide (secreted and
transmembrane). The PRO protein, and PRO agonists, PRO antagonists or
anti-PRO antibodies are useful for preparation of a medicament useful in
the treatment of a condition which is responsive to the PRO protein,
agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
employed as molecular weight markers for protein electrophoresis. The PRO
coding sequence has applications in molecular biology, including use as
hybridisation probes, and in chromosome and gene mapping.

Sequence 119 AA;

Query Match 100.0%; Score 644; DB 22; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.8e-66;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVLISLLLLPLMLSMVSSSLNPGVARGHRDGOASRRWLQEGQCECKDWFRLAP 60
|||||
1 MKVLISLLLLPLMLSMVSSSLNPGVARGHRDGOASRRWLQEGQCECKDWFRLAP 60
|||||

QY 61 RRKFTVSLPKKQPCDHFKNVKKTRHQRHHRKPNKHSRACQFLKQCQLRSFALPL 119
|||||
Db 61 RRKFTVSLPKKQPCDHFKNVKKTRHQRHHRKPNKHSRACQFLKQCQLRSFALPL 119
|||||

RESULT 8
AAB65191
AAB65191 standard; Protein; 119 AA.
XX AAB65191;

XX 02-APR-2001 (first entry)
XX Human PRO842 (UNQ473) protein sequence SEQ ID NO:165.

XX Human; secreted and transmembrane protein; PRO; cytostatic;
cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
diagnostic assay.

XX Homo sapiens.
XX WO200073454-A1. — *US 661*
XX 07-DEC-2000.

XX 30-MAR-2000; 2000WO-US08439.
XX 02-JUN-1999; 99WO-US12252.
XX 23-JUN-1999; 99US-0141037.
XX 07-JUL-1999; 99US-0143048.
XX 20-JUL-1999; 99US-0144758.
XX 26-JUL-1999; 99US-0145698.
XX 28-JUL-1999; 99US-0146222.
XX 17-AUG-1999; 99US-0149396.
XX 15-SEP-1999; 99WO-US21090.
XX 15-SEP-1999; 99WO-US21547.
XX 08-OCT-1999; 99US-0158663.
XX 30-NOV-1999; 99WO-US28313.
XX 01-DEC-1999; 99WO-US28301.
XX 16-DEC-1999; 99WO-US30095.
XX 20-DEC-1999; 99WO-US30911.
XX 05-JAN-2000; 2000WO-US00219.
XX 06-JAN-2000; 2000WO-US00376.
XX 11-FEB-2000; 2000WO-US03565.
XX 18-FEB-2000; 2000WO-US04341.
XX 22-FEB-2000; 2000WO-US04414.
XX 24-FEB-2000; 2000WO-US04914.
XX 24-FEB-2000; 2000WO-US05004.
XX 02-MAR-2000; 2000WO-US05841.
XX 15-MAR-2000; 2000WO-US06884.
XX 20-MAR-2000; 2000WO-US07377.

(GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
XX Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi CJ, Gurney AL, Kijavini JJ, Napier MA, Pan J, Paoni NF;
XX Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
XX Zhang Z;
XX WPI: 2001-032160/04.
XX N-PSDB; AAF44147.

XX PRO polynucleotides used to produce polypeptides used to target
XX bioactive molecules such as toxins, radiolabels or antibodies, to
XX specific cells, to cause targeted cell death -
XX Claim 12; Fig 99; 935pp; English.

XX The present invention describes human secreted and transmembrane PRO
XX proteins. The PRO proteins have cytostatic activity. The PRO proteins
XX can be used for targeted delivery of bioactive molecules, such as
XX toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide

sequences, and their fragments, can be used as hybridisation probes, in chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents, the PRO nucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to AAF44470 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to AAB65300 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.

Sequence 119 AA:

Query Match	100.0%	Score 644:	DB 22:	Length 119;
Best Local Similarity	100.0%;	Pred. No. 1.8e-66;		
Matches 119;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
1	MKVLISSLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGQCECKDWFLRAP	60		
1	MKVLISSLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGQCECKDWFLRAP	60		
61	RRRFMTVSLGPKKQPCDHFKNVKKTRQHRHKKPNKHSRAQQQFLKQQLRSFALPL	119		
61	RRRFMTVSLGPKKQPCDHFKNVKKTRQHRHKKPNKHSRAQQQFLKQQLRSFALPL	119		

SULT 9
P54931
ABP54931 standard; Protein; 119 AA.

ABP54931;

08-JAN-2003 (first entry)

Human cytokine PRO842 (CK27);

PRO842; chemokine; human; antiinflammatory; dermatological; hepatotropic; antiallergic; antiasthmatic; immunosuppressive; antithroid; antidiabetic; antianaemic; haemostatic; antipsoriatic; antirheumatic; antiatriatic; nephrotropic.

Homo sapiens.

Key	Location/Qualifiers
Peptide	1..22
	/label= Signal_peptide
Protein	23..119
	/label= Mature_protein
Modified-site	27..32
	/note= "potential N-myristoylation site"
Modified-site	39..41
	/note= "potential protein kinase C phosphorylation site"
Modified-site	46..51
	/note= "potential N-myristoylation site"

WO200270706-A2.

12-SEP-2002

07-DEC-2007: 2001WC-US48060

28-FEB-2001: 2001WO-US06520

28-FEB-2001; 2001WO-0506320.
28-AUG-2001: 2001US-0941992.

CEPH \ GENENTECH INC

French D. Crimaldi JC. Hillian K.T. Pisabarro MT. Schmidt KN:

FRENCH D, GRIMAUD JC, HILLAN KS, FISABATTO MI, SCHMIDT KN,
SMITH V, THOMAS D, VANDJEN RL, WATANABE CK, WILLIAMS PM, WOOD WI;

WPT: 2002-750461/91

WPI; 2002-730461/
N-PSDB: ABV73914

New PR0842 polypeptides having structural homology to interleukin-8, useful for treating or diagnosing a mammal with an inflammatory disease or immune related disease, e.g. rheumatoid arthritis, osteoarthritis or allergic disease.

Claim 1: Fig 2: 118pp: English.

The present sequence is the protein sequence of PR0842 (CK27), a novel human chemokine (mol.wt. 13.8 Kda, PI 11.16) having structural homology to interleukin-8. Microarray analysis has shown PR0842 to be over-expressed in colon tumour, lung tumour and breast tumour cells compared with non-cancerous human tissue, making it a useful diagnostic marker for cancerous tumours and a therapeutic target. PR0842 also plays a role in the inflammatory response, having chemoattractant properties toward monocytes and dendritic cells. The invention provides PR0842 polypeptides, polynucleotides, host cells, vectors and antibodies, as well as methods of treating an immune related disorder by using a PR0842 polypeptide, or an agonist, antagonist or antibody. The immune related disorder may be systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthritis, systemic sclerosis, idiopathic inflammatory myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating disease of the central or peripheral nervous system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome, chronic inflammatory demyelinating polyneuropathy, hepatobiliary disease, infectious or autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's disease, an autoimmune or immune-mediated skin disease, a bullous skin disease, erythema multiforme, contact dermatitis, psoriasis, an allergic disease, asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity, urticaria, an immunologic disease of the ovum, an immunologic disease of the lung, eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, a transplantation associated disease, graft rejection or graft-versus-host-disease (all claimed).

Sequence 119 AA:

ery Match	100.0%	Score 644;	DB 23;	Length 119;
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very Match
1st local similarity

ts local similarity	100.00%	Mismatches	0;	Indels	0;	Gaps	0;	
tches 119:	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;

1 MKVLISSLLLLPLMLSMVSSSLNPGVARGHRDRGQASRRWLQEGGQCECECKDWFLRAP 60

1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGQCECECKDWFLRAP 60

61 RRKFM TVSG L P K K O C P C D H F K G N V K K T R H Q R H R K P N K H S R A C Q Q F L K Q C Q L R S F A L P L 119

67 RRKEMTVSGLPKKOCPCDHFKGNVKKTTRHQRHHRKPNKHSRACQQLKQCQLRSFALPL 119

RESULT 10

RESOLVED IN
ABG95863

ABG95863
ID ABG95863 standard; Protein; 119 AA.

AA
AC ABG95863;

AA	10-DEC-2002	(first entry)
DT		

Human secreted/transmembrane protein PR0842.

Human: secreted protein; transmembrane protein; antirheumatic;
 KW

antiarthritic; osteopathic; sports-related joint problem; KW

articular cartilage defect; osteoarthritis; rheumatoid arthritis.

OS Homo sapiens.

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29-AUG-2002.
 06-DEC-2001; 2001US-0006867.
 29-OCT-1997; 97US-063435P.
 29-OCT-1997; 97US-064215P.
 22-APR-1998; 98US-082797P.
 29-APR-1998; 98US-083495P.
 15-MAY-1998; 98US-085579P.
 10-JUN-1998; 98US-088811P.
 10-JUN-1998; 98US-088824P.
 10-JUN-1998; 98US-088825P.
 11-JUN-1998; 98US-088863P.
 12-JUN-1998; 98US-089105P.
 16-JUN-1998; 98US-089514P.
 16-SEP-1998; 99WO-US19330.
 08-MAR-1999; 99WO-US05028.
 14-MAY-1999; 99WO-US10733.
 02-JUN-1999; 99WO-US12252.
 01-SEP-1999; 99WO-US20111.
 15-SEP-1999; 99WO-US21090.
 15-SEP-1999; 99WO-US21194.
 22-DEC-1999; 99WO-US0720.
 18-FEB-2000; 2000WO-US04341.
 18-FEB-2000; 2000WO-US04342.
 30-MAR-2000; 2000WO-US08439.
 22-MAY-2000; 2000WO-US14042.
 02-JUN-2000; 2000WO-US15264.
 23-AUG-2000; 2000WO-US23522.
 24-AUG-2000; 2000WO-US23328.
 10-NOV-2000; 2000WO-US30873.
 01-DEC-2000; 2000WO-US32378.
 20-DEC-2000; 2000WO-US34956.
 28-FEB-2001; 2001WO-US06520.
 20-JUN-2001; 2001WO-US19692.
 29-JUN-2001; 2001WO-US21066.
 09-JUL-2001; 2001WO-US21735.
 (GETH) GENENTECH INC.

Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
 WPI: 2002-731348/79.
 N-PSDB; ABS74390.

New isolated secreted and transmembrane PRO polypeptide useful for
 modulating biological activity of a cell, or for treating
 sports-related joint problems, osteoarthritis or rheumatoid arthritis

Claim 20; Fig 26; 399pp; English.

The invention relates to an isolated secreted and transmembrane PRO
 polypeptide having 80 % sequence identity to a sequence appearing
 as ABG5851-ABG95934 or their associated signal peptide, or a sequence of
 an extracellular domain of the proteins with their associated signal
 peptide or lacking its associated signal peptide. Also included are
 the nucleic acids encoding the proteins, vectors, host cells,
 fusion proteins and antibodies which specifically bind to the proteins.
 The proteins are useful for detecting a polypeptide designated as A, B, C
 or D in a sample suspected of containing an A, B, C or D polypeptide,
 by contacting the sample with a polypeptide designated as E, F, G, H or
 I (or vice versa) and determining the formation of a A/E, B/F, C/H
 or D/I polypeptide conjugate in the sample, where the formation of the
 conjugate is indicative of the presence of an A, B, C or D polypeptide
 in the sample, where A is a PRO10272 polypeptide, B is a PRO20110
 polypeptide, C is a PRO10096 polypeptide, D is a PRO19760 polypeptide,
 E is a PRO5801 polypeptide, F is a PRO1 polypeptide, G is a PRO20040
 polypeptide, H is a PRO20233 polypeptide and I is a PRO1890
 polypeptide. The sample comprises a cell suspected of expressing the A,
 B, C or D polypeptide. The E, F, G, H or I polypeptide is labeled with
 a detectable label or is attached to a solid support. The proteins are
 useful for linking a bioactive molecule to a cell expressing a

polypeptide designated as A, B, C or D or E, F, G, H or I. The bioactive
 molecule is a toxin, a radiolabel or an antibody. The bioactive molecule
 causes death of the cell. A, B, C, D, E, F, G, H, or I, or antibodies
 against them are useful for modulating a biological activity of a cell
 expressing a polypeptide designated as A, B, C or D or E, F, G, H, or
 I. The cell is killed. The proteins are useful for identifying
 agonists or antagonists, for the preparation of a medicament useful in
 the treatment of a condition which is responsive to the proteins, as
 molecular weight markers for protein electrophoresis purposes, and as
 therapeutic agents for treating sports-related joint problems,
 articular cartilage defects, osteoarthritis or rheumatoid arthritis.
 Nucleic acids encoding the proteins are useful as hybridisation probes,
 in chromosome and gene mapping, in the generation of anti-sense RNA and
 DNA, for the preparation of the proteins, to generate transgenic or
 knockout animals which are useful in the development and screening of
 therapeutic useful reagents, for chromosome identification, and in gene
 therapy. The antibody is useful as a therapeutic agent, in a diagnostic
 assay and for affinity purification of the protein from recombinant
 cell culture natural sources. The present sequence represents a novel
 secreted or transmembrane protein of the invention.

XX Sequence 119 AA;

Query Match 100.0%; Score 644; DB 23; Length 119;
 Best Local Similarity 100.0%; Pred. No. 1.8e-66;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVLISLILLPLMLSMVSSSLNPGVARGHRRDQASRRWLQEGGQCECKDWFRLAP 60
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 DB 1 MKVLISLILLPLMLSMVSSSLNPGVARGHRRDQASRRWLQEGGQCECKDWFRLAP 60
 |||||
 QY 61 RRKPTVSGLPKKQPCDHFHKGKGNVKTTRHQRHRRKPKNSRACQFLKCCQLRSFALPL 119
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 DB 61 RRKPTVSGLPKKQPCDHFHKGKGNVKTTRHQRHRRKPKNSRACQFLKCCQLRSFALPL 119
 |||||

RESULT 11

ABU071181 ID ABU071181 standard; Protein; 119 AA.
 XX AC ABU071181;
 XX AC ABU071181;
 DT 10-JUN-2003 (first entry)
 XX DE Human PRO842 protein.
 XX KW Human; PRO; secreted; transmembrane; cytostatic; TNF-alpha; blood;
 KW tumour necrosis factor alpha release; chondrocyte cell; proliferation;
 XX differentiation; tumour; gene therapy.
 OS Homo sapiens.
 XX US2003036143-A1.
 PN US2003036143-A1.
 XX 20-FEB-2003.
 XX 02-JUL-2002; 2002US-0187600.
 XX 16-SEP-1998; 98WO-US19330.
 PR 07-OCT-1998; 98WO-US21141.
 PR 01-DEC-1998; 98WO-US25108.
 PR 08-MAR-1999; 99WO-US05028.
 PR 14-MAY-1999; 99WO-US10733.
 PR 02-JUN-1999; 99WO-US12252.
 PR 01-SEP-1999; 99WO-US20111.
 PR 15-SEP-1999; 99WO-US21090.
 PR 01-DEC-1999; 99WO-US28301.
 PR 02-DEC-1999; 99WO-US28551.
 PR 30-DEC-1999; 99WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.

24-FEB-2000; 2000WO-US05004.
01-MAR-2000; 2000WO-US05601.
02-MAR-2000; 2000WO-US05841.
15-MAR-2000; 2000WO-US06884.
30-MAR-2000; 2000WO-US08439.
17-MAY-2000; 2000WO-US13705.
22-MAY-2000; 2000WO-US14042.
30-MAY-2000; 2000WO-US14941.
02-JUN-2000; 2000WO-US15264.
28-JUL-2000; 2000WO-US20710.
04-AUG-2000; 2000WO-US23328.
28-NOV-2000; 2000WO-US30952.
01-DEC-2000; 2000WO-US32678.
20-DEC-2000; 2000WO-US34956.
28-FEB-2001; 2001WO-US06520.
01-JUN-2001; 2001WO-US17800.
20-JUN-2001; 2001WO-US19692.
29-JUN-2001; 2001WO-US21066.
09-JUL-2001; 2001WO-US21735.
29-AUG-2001; 2001WO-US27099.
18-SEP-1997; 97US-052623P.
18-SEP-1997; 97US-052685P.
17-OCT-1997; 97US-062250P.
21-OCT-1997; 97US-063486P.
24-OCT-1997; 97US-063120P.
24-OCT-1997; 97US-063121P.
28-OCT-1997; 97US-063540P.
28-OCT-1997; 97US-063541P.
28-OCT-1997; 97US-063544P.
28-OCT-1997; 97US-063564P.
29-OCT-1997; 97US-063734P.
31-OCT-1997; 97US-063870P.
31-OCT-1997; 97US-064103P.
13-NOV-1997; 97US-065311P.
21-NOV-1997; 97US-066120P.
24-NOV-1997; 97US-066466P.
24-NOV-1997; 97US-066772P.
11-DEC-1997; 97US-069335P.
12-DEC-1997; 97US-069425P.
17-DEC-1997; 97US-069870P.
18-DEC-1997; 97US-068017P.
10-MAR-1998; 98US-077450P.
11-MAR-1998; 98US-077632P.
11-MAR-1998; 98US-077649P.
20-MAR-1998; 98US-078886P.
20-MAR-1998; 98US-078939P.
27-MAR-1998; 98US-079664P.
31-MAR-1998; 98US-079785P.
31-MAR-1998; 98US-080107P.
01-APR-1998; 98US-080194P.
01-APR-1998; 98US-080327P.
01-APR-1998; 98US-080333P.
08-APR-1998; 98US-081049P.
08-APR-1998; 98US-081070P.
09-APR-1998; 98US-081195P.
15-APR-1998; 98US-081838P.
21-APR-1998; 98US-082568P.
21-APR-1998; 98US-082569P.
22-APR-1998; 98US-082704P.
22-APR-1998; 98US-082797P.
28-APR-1998; 98US-083322P.
29-APR-1998; 98US-083495P.
29-APR-1998; 98US-083496P.
29-APR-1998; 98US-083499P.
23-APR-1998; 98US-083559P.
03-MAY-1998; 98US-084366P.
06-MAY-1998; 98US-084414P.
07-MAY-1998; 98US-084639P.
07-MAY-1998; 98US-084640P.
07-MAY-1998; 98US-084643P.
15-MAY-1998; 98US-085579P.
15-MAY-1998; 98US-085580P.
15-MAY-1998; 98US-085582P.

PR 15-MAY-1998; 98US-085700P.
PR 18-MAY-1998; 98US-086023P.
PR 22-MAY-1998; 98US-086392P.
PR 22-MAY-1998; 98US-086486P.
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PR 10-JUN-1998; 98US-088826P.
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PR 11-JUN-1998; 98US-088863P.
PR 11-JUN-1998; 98US-088876P.
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PR 17-JUN-1998; 98US-089598P.
PR 17-JUN-1998; 98US-089653P.
PR 18-JUN-1998; 98US-089908P.
PR 19-JUN-1998; 98US-089952P.
PR 22-JUN-1998; 98US-090246P.
PR 22-JUN-1998; 98US-090252P.
PR 22-JUN-1998; 98US-090254P.
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PR 26-JUN-1998; 98US-090863P.
PR 26-JUN-1998; 98US-091010P.
PR 01-JUL-1998; 98US-091359P.
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PR 10-AUG-1998; 98US-096012P.
PR 17-AUG-1998; 98US-096757P.
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PR 17-AUG-1998; 98US-096891P.
PR 17-AUG-1998; 98US-096897P.

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26-AUG-1998; 98US-097955P.
26-AUG-1998; 98US-097971P.
26-AUG-1998; 98US-097974P.
26-AUG-1998; 98US-098014P.
01-SEP-1998; 98US-098716P.
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02-SEP-1998; 98US-098843P.
09-SEP-1998; 98US-099602P.
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Best Local Similarity 100.0%; Pred. No. 1.8e-66;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKYLISLLLLPLMLMSVSSSLNPGVARGHRDQASRRWLQGGQCECKDWFRLAP 60
1 MKYLISLLLLPLMLMSVSSSLNPGVARGHRDQASRRWLQGGQCECKDWFRLAP 60
61 RRKFTVSGLPKKQPCDHFPGKGNVKKTRHQHRRKPNKHSRACQOFLKQCQLRSFALPL 119
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SUITE 12
071518
ABU71518 standard; Protein; 119 AA.
ABU71518;
10-JUN-2003 (first entry)
Human secreted polypeptide PRO842.
Human; gene therapy; tumour; cancer.
Homo sapiens.
US2003013855-A1.
16-JAN-2003.
03-MAY-2002; 2002US-0063616.
30-DEC-1998; 98KR-0062142.
08-MAR-1999; 99WO-US05028.
14-MAY-1999; 99WO-US10733.
30-DEC-1999; 99WO-US12173.
18-FEB-2000; 2000WO-US04341.
01-MAR-2000; 2000WO-US05601.
02-MAR-2000; 2000WO-US05841.
21-MAR-2000; 2000WO-US07532.
22-MAY-2000; 2000WO-US14042.
02-JUN-2000; 2000WO-US15264.
24-AUG-2000; 2000WO-US23328.
10-NOV-2000; 2000WO-US30873.
01-DEC-2000; 2000WO-US32678.
20-DEC-2000; 2000WO-US34956.
28-FEB-2001; 2001WO-US06520.
01-JUN-2001; 2001WO-US17800.
14-MAY-1999; 99US-0311832.
25-AUG-1999; 99US-0380137.
25-AUG-1999; 99US-0380138.
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25-AUG-1999; 99US-0380142.
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12-NOV-1999; 99US-0423844.
22-AUG-2000; 2000US-0644848.
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18-SEP-2000; 2000US-0665350.
08-NOV-2000; 2000US-0709238.
20-DEC-2000; 2000US-0747259.
22-MAR-2001; 2001US-0816744.
10-MAY-2001; 2001US-0854208.
10-MAY-2001; 2001US-0854280.
30-MAY-2001; 2001US-0870574.
03-JUN-2001; 2001US-0874503.
29-JUN-2001; 2001US-0869599.
18-JUL-2001; 2001US-0908827.
06-DEC-2001; 2001US-0006867.
XX
PA (GETH ) GENENTECH INC.
XX
XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
XX WPI; 2003-330485/31.
XX N-PSDB; ACA58822.
XX
XX New isolated antibody specifically binding a PRO polypeptide, useful
XX for the preparation of a medicament for treating disorders with the
XX aberrant expression or activity of the PRO polypeptide, such as tumor
XX conditions and cancer -
XX
XX Disclosure; Page 93; 406pp; English.
XX
XX The invention relates to an antibody that binds to a polypeptide with a
XX fully defined sequence given in the specification. The methods and
XX compositions (containing antibodies that specifically bind a PRO
XX polypeptide) of the present invention are useful for the preparation of a
XX medicament for the treatment of disorders associated with the aberrant
XX expression or activity of the PRO polypeptide, such as tumour conditions
XX and cancer. They can also be used to generate transgenic or knockout
XX animals useful in the development and screening of therapeutically useful
XX reagents. The PRO polypeptides and encoding nucleic acids can be used as
XX molecular weight markers for protein electrophoresis, chromosome
XX identification and tissue typing. The PRO polypeptides are useful to
XX induce angiogenesis e.g wound healing; in the treatment of sports-related
XX joint problems, articular cartilage defects, osteoarthritis or rheumatoid
XX arthritis; diabetes; hyperinsulinaemia and hypoinsulinaemia. The
XX antibodies may be used in various diagnostic, competitive binding and/or
XX immunoprecipitation assays. The present sequence represents the amino
XX acid sequence of a PRO polypeptide of the invention.
XX
XX Query Match 100.0%; Score 644; DB 24; Length 119;
XX Best Local Similarity 100.0%; Pred. No. 1.8e-66;
XX Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX
XX DB 1 MKYLISLLLLPLMLMSVSSSLNPGVARGHRDQASRRWLQGGQCECKDWFRLAP 60
XX
XX QY 61 RRKFTVSGLPKKQPCDHFPGKGNVKKTRHQHRRKPNKHSRACQOFLKQCQLRSFALPL 119
XX
XX DB 61 RRKFTVSGLPKKQPCDHFPGKGNVKKTRHQHRRKPNKHSRACQOFLKQCQLRSFALPL 119
XX
XX
XX RESULT 13
XX ABU71964
XX ID ABU71964 standard; Protein; 119 AA.
XX
XX AC ABU71964;
XX
XX DT 11-JUN-2003 (first entry)
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Novel human secreted and transmembrane protein PR0842.

Human; secreted and transmembrane polypeptide;
 chromosome mapping; gene mapping; transgenic animal; knockout animal;
 therapeutic agent screening; chromosome identification; tissue typing;
 gene therapy.

Homo sapiens.

US2003018183-A1.

23-JAN-2003.

01-MAY-2002; 2002US-0063512.

06-DEC-2001; 2001US-0006867.

(GETH) GENENTECH INC.

Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;

WPI: 2003-330984/31.
 N-PSDB: ACA60375.

New secreted and transmembrane PRO polypeptides and nucleic acid
 molecules encoding the polypeptides, useful in gene therapy or
 preparing a medicament for treating a condition that is responsive to
 the PRO polypeptide or antibody.

Disclosure; Fig 26; 409pp; English.

The invention describes novel isolated PRO polypeptides. The PRO
 polypeptides or anti-PRO antibodies are useful in preparing a medicament
 for treating a condition that is responsive to the PRO polypeptide or
 antibody. The PRO nucleotide sequences may be used as hybridisation
 probes in chromosome and gene mapping, or in generating antisense RNA
 and DNA. PRO nucleic acids are also useful in preparing PRO polypeptides,
 in assays to identify other proteins or molecules involved in binding
 reaction, to generate transgenic animals or knockout animals, which in
 turn are useful in the development and screening of therapeutically
 useful reagents, for chromosome identification, and tissue typing. The
 PRO polypeptides and nucleic acid molecules are also useful in gene
 therapy, and as molecular weight markers for protein electrophoresis
 purposes. The anti-PRO antibodies may be used in diagnostic assays for
 PRO, or for the affinity purification of PRO from recombinant cell
 culture or natural sources. This is the amino acid sequence of a novel
 human secreted and transmembrane PRO polypeptide.

Sequence 119 AA;

Query Match 100.0%; Score 644; DB 24; Length 119;
 Best Local Similarity 100.0%; Pred. No. 1.8e-66;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDQASRRWLQEGGQCECKDWFRLAP 60
 b 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDQASRRWLQEGGQCECKDWFRLAP 60
 Y 61 RRKFMVSGLPKKQPCDHFHKGKGVKTRHQRHRRKPNKHSRACQQLKQCLRSFALPL 119
 b 61 RRKFMVSGLPKKQPCDHFHKGKGVKTRHQRHRRKPNKHSRACQQLKQCLRSFALPL 119

RESULT 14

BU72121
 D ABU72121 standard; Protein: 119 AA.

X C ABU72121;

X T 13-JUN-2003 (first entry)

X

DE Human PRO polypeptide #13.
 XX Human; PRO polypeptide; secreted and transmembrane protein;
 KW anti-PRO antibody; diagnostic assay; gene expression.
 XX Homo sapiens.
 OS US2003023042-A1.
 PN 30-JAN-2003.
 PD 01-MAY-2002; 2002US-0063502.
 PP 06-DEC-2001; 2001US-0006867.
 PR (GETH) GENENTECH INC.
 PA Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
 XX WPI: 2003-331484/31.
 DR N-PSDB: ACA63385.
 XX Novel monoclonal antibody that binds to secreted and transmembrane
 PT polypeptide, useful for detecting and purifying the polypeptide and
 PT also for treating conditions responsive to the antibody.
 PS Disclosure; Fig 26; 408pp; English.

CC The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The
 CC PRO polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides and polynucleotides are useful for preparing a
 CC medicament useful in the treatment of a condition responsive to
 CC anti-PRO antibody. Anti-PRO antibodies are useful in diagnostic
 CC assays for PRO, by detecting its expression in specific cells,
 CC tissues or serum, and for affinity purification of PRO from
 CC recombinant cell culture or natural sources. ABU72109-ABU72192
 CC represent the human PRO polypeptides of the invention.
 XX Sequence 119 AA;

Query Match 100.0%; Score 644; DB 24; Length 119;
 Best Local Similarity 100.0%; Pred. No. 1.8e-66;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDQASRRWLQEGGQCECKDWFRLAP 60
 Db 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDQASRRWLQEGGQCECKDWFRLAP 60
 QY 61 RRKFMVSGLPKKQPCDHFHKGKGVKTRHQRHRRKPNKHSRACQQLKQCLRSFALPL 119
 Db 61 RRKFMVSGLPKKQPCDHFHKGKGVKTRHQRHRRKPNKHSRACQQLKQCLRSFALPL 119

RESULT 15

ABU65638
 ID ABU65638 standard; Protein: 119 AA.

XX AC ABU65638;

XX DT 19-MAY-2003 (first entry)

XX DE Human secreted/transmembrane protein, SEQ ID 140.

XX KW Human; PRO; secreted protein; transmembrane protein;
 KW cystostatic; antiarthritic; osteopathic; adrenal tumour; lung tumour;
 KW colon tumour; breast tumour; prostate tumour; rectal tumour;
 KW cervical tumour; liver tumour; TNF-alpha release; arthritis;
 KW tumour necrosis factor alpha; chondrocyte cell; bone disorder;
 KW cartilage disorder; sports injury.

XX OS Homo sapiens.

US2003036156-A1.
20-FEB-2003.
02-JUL-2002; 2002US-0188767.
16-SEP-1998; 98WO-US19330.
07-OCT-1998; 98WO-US21141.
01-DEC-1998; 98WO-US21108.
08-MAR-1999; 99WO-US05028.
14-MAY-1999; 99WO-US10733.
02-JUN-1999; 99WO-US12252.
01-SEP-1999; 99WO-US20111.
15-SEP-1999; 99WO-US21090.
01-DEC-1999; 99WO-US28301.
02-DEC-1999; 99WO-US28551.
30-DEC-1999; 99WO-US31274.
03-JAN-2000; 2000WO-US00219.
18-FEB-2000; 2000WO-US04341.
18-FEB-2000; 2000WO-US04342.
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01-MAR-2000; 2000WO-US05601.
02-MAR-2000; 2000WO-US05841.
15-MAR-2000; 2000WO-US06884.
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20-DEC-2000; 2000WO-US34956.
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02-JUN-1998; 98US-087609P.
02-JUN-1998; 98US-087759P.
03-JUN-1998; 98US-087827P.
04-JUN-1998; 98US-088025P.
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11-JUN-1998; 98US-088861P.
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12-JUN-1998; 98US-089050P.
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16-JUN-1998; 98US-089512P.
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26-JUN-1998;	98US-090863P.		
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01-SEP-1998;	98US-098716P.		
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10-SEP-1998;	98US-099741P.		
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61 RRKEMTVSLPKKQCCPDHFKNVKKTRHQRRHKPNKHSRAQQQLKQCLRSFALPL	119		
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arch completed: September 13, 2003, 14:43:47
b time : 55.6667 secs

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2	77	12.0	2269	1	QJ1750	genome polyprotein	
3	74.5	11.6	448	2	I50451	vitamin D receptor	
4	73.5	11.4	70	2	A60912	vitamin D receptor	
5	71.5	11.1	108	2	G84522	similar to gibbere	
6	71	11.0	411	2	S35333	steroid receptor p	
7	71	11.0	2262	2	S16664	large protein L -	
8	71	11.0	3190	2	TJ1828	CRAB-binding prote	
9	70.5	10.9	1283	2	T49804	hypothetical prote	
10	70.5	10.9	543	2	A32693	steroid receptor p	
11	70	10.9	746	2	B32693	steroid receptor p	
12	70	10.9	1095	2	T24061	hypothetical prote	
13	70	10.9	1620	2	T27283	hypothetical prote	
14	69.5	10.8	221	2	C34768	ORE2 protein - Orf	
15	69.5	10.8	575	1	TH4D8	thrombomodulin pre	
16	69	10.7	200	2	C83086	hypothetical prote	
17	68.5	10.6	381	2	A46358	steroid/thyroid ho	
18	68.5	10.6	422	2	PC4019	vitamin D receptor	
19	68.5	10.6	423	2	S11761	1,25-dihydroxyvita	
20	68.5	10.6	427	2	A28200	vitamin D receptor	
21	68.5	10.6	427	2	S24174	vitamin D receptor	
22	68.5	10.6	647	2	S36557	E1 protein - human	
23	68.5	10.6	1006	2	S74992	hypothetical prote	
24	68	10.6	283	2	S42933	G-box-binding prot	
25	67	10.4	376	2	T48950	cysteine proteinase	
26	67	10.4	475	2	B69643	histidine permease	
27	67	10.4	1062	2	T14151	Inv protein - mous	
28	67	10.4	1062	2	T30355	inversin - mouse	
29	66.5	10.3	103	2	A72713	hypothetical prote	

```
F;1-70/Domain: erba transforming protein homology (fragment) <ERBA>

Query Match      11.4%; Score 73.5; DB 2; Length 70;
Best Local Similarity 35.5%; Pred. No.1.1;
Matches 22; Conservative 9; Mismatches 12; Indels 19; Gaps 5;

QY    50 CE-CKDWFLRAPRKEMTVSGGLPKKCPDHFPGNKKTRHORHHRKPKNKSRACQOFLK 108
      |||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db     20 CEGCKGFFRRSMKRKAFT-----CP---FNGDCIKTKDNR-----RHQQACR-LK 61

QY    109 QG 110
      ::
Db     62 RC 63

RESULT 5
G84522
similar to gibberellin-regulated proteins [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 01-Mar-2002
C;Accession: G84522
M.;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: G84522
A>Status: preliminary
A:Molecule type: DNA
A;Residues: 1-108 <STO>
A;Cross-references: GB:AE002093; MID:g3650032; PIDN:AAC61287.1; GSFPDB:GN00139
C;Genetics:
A;Gene: At2g14900
A;Map position: 2
C;Superfamily: gibberellin-regulated protein GASA2

Query Match      11.1%; Score 71.5; DB 2; Length 108;
Best Local Similarity 25.9%; Pred. No.2.7;
Matches 29; Conservative 18; Mismatches 38; Indels 27; Gaps 7;

QY    1 MKVLISLLLL-LPLMLMSVSSSLNPGVARG-----HRDRGQAASRWLQGGQECE-- 51
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db     1 MKIIVSILVLALLLSSSLASATISDAFGSAVAFAPOSKDGPALEKWC---GQKEGR 57

QY    52 CKDWFLRAPRKEMTVSGGLPKKCPDHFPGNKKTRHORHHRKPKNKSRAC 103
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db     58 CKE---AGMKDRGLKYCGIOCKDCQC-----YPSGT-----GNKHECAC 94

RESULT 6
S35333
steroid receptor protein svp44 - zebra fish
C;Species: Brachydanio rerio (zebra fish)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 24-Sep-1999
C;Accession: S35333
R;Fjose, A.; Norne, S.; Weber, U.; Mlodzik, M.
EMBO J. 12, 1403-1414, 1993
A;Title: Functional conservation of vertebrate seven-up related genes in neurogenesis
A;Reference number: S35333; MUID:93223680; PMID:8467797
A;Accession: S35333
A:Molecule type: mRNA
A;Residues: 1-411 <FOU>
A;Cross-references: EMBL:X70299; MID:g296418; PIDN:CAA49780.1; PID:g296419
C;Genetics:
A;Gene: svp44
C;Superfamily: unassigned erba-related proteins; erba transforming protein homology
C;Keywords: DNA binding; steroid hormone receptor; zinc finger
F;74-320/Domain: erba transforming protein homology <ERBA>
F;75-96/Region: zinc finger
F;112-136/Region: zinc finger

Query Match      11.0%; Score 71; DB 2; Length 411;
```

Db 2430 QHTKNCK--RKPNGGCPICKQLIALC 2453

RESULT 9
T49804
hypothetical protein B11B22.60 [imported] - Neurospora crassa
C:Species: Neurospora crassa
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C:Accession: T49804
R:Schulte, U.; Algn. V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatu
submitted to the Protein Sequence Database, May 2000
A:Reference number: Z25022
A:Accession: T49804
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1283 <SCH>
A:Cross-references: EMBL:AL356834; GSPDB:GN00116; NCSP:B11B22.60
A:Experimental source: BAC clone B11B22; strain OR74A
C:Genetics:
A:Gene: NCSP:B11B22.60
A:Map position: 6
A:Introns: 856/2

Query Match 10.9%; Score 70.5; DB 2; Length 1283;
Best Local Similarity 24.5%; Pred. No. 29;
Matches 26; Conservative 18; Mismatches 31; Indels 31; Gaps 6;

QY 33 RDRGQASRRWLQGGQCECKDNFLAPRKFKMTVS---GLPKKQCPDHFPGKNVKK--T 87
Db 454 RNNKMKKKQKQKQKGGSGSK-----LRAPSAMPVPVYVWGSPSRAPWPLRWGHIIRNGDV 508

QY 88 RHQRHHR-----KPNKHSRACQF--LKQCQLRSEA 116
Db 509 GHSHNQHMVDEGYVRLWSEKLEPH---QQFARLRKAELALYA 550

RESULT 10
A32693
steroid receptor protein svp 1 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 20-Sep-1999
C:Accession: A32693
R:Modzik, M.; Hiromi, Y.; Weber, U.; Goodman, C.S.; Rubin, G.M.
Cell 60, 211-224, 1990
A:Title: The Drosophila seven-up gene, a member of the steroid receptor gene superfamily
A:Reference number: A32693; MUID:90124631; PMID:2105166
A:Accession: A32693
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-543 <MLO>
A:Cross-references: GB:M28963; NID:g158518; PIDN:AAA62770.1; PID:g158519.
C:Genetics:
A:Gene: FlyBase:svp
A:Cross-references: FlyBase:FBgn0003651
C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
C:Keywords: alternative splicing; DNA binding; steroid hormone receptor; transcription
E:198-452/Domain: erba transforming protein homology <ERBA>
E:200-220/Region: zinc finger
E:236-260/Region: zinc finger

Query Match 10.9%; Score 70; DB 2; Length 543;
Best Local Similarity 26.7%; Pred. No. 16;
Matches 27; Conservative 12; Mismatches 28; Indels 34; Gaps 5;

QY 21 SSSLNPG-----VARGHRRGQASRRWLQGGQCECKDNFLAPRKFKMTVS 69
Db 183 SOSNSSSQSDSKONIECVGDKSSKHHVQQTCEG-----CKSFPRSVRRN-LTYS 236

QY 70 LPKKQCCPDHFPGKNVKKTRHQRHHRKPNKHSRACQQLKOC 110
Db 237 RGRNRCPTD-----QHRNOCQVCR-----LKKC 260

SULT 11
2593
eroid receptor protein svp 2 - fruit fly (Drosophila melanogaster)
Species: Drosophila melanogaster
Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 12-Sep-1997
Accession: B32693
Miodzik, M.; Hironi, Y.; Weber, U.; Goodman, C.S.; Rubin, G.M.
11 60, 211-224, 1990
Title: The Drosophila seven-up gene, a member of the steroid receptor gene superfamily
Reference number: A32693; MUID:90124631; PMID:2105166
Accession: B32693
Status: preliminary
Molecule type: mRNA
Residues: 1-746 <MLO>
Cross-references: GB:M28863; GB:M28864
Genetics:
3one: FlyBase:svp
Cross-references: FlyBase:FBgn0003651
Superfamily: unassigned erba-related proteins; erba transforming protein homology
Keywords: alternative splicing; DNA binding; steroid hormone receptor; transcription
198-452/Domain: erba transforming protein homology <ERBA>
200-220/Region: zinc finger
236-260/Region: zinc finger
Query Match 10.9%; Score 70; DB 2; Length 746;
Best Local Similarity 26.7%; Pred. No. 21;
Matches 27; Conservative 12; Mismatches 28; Indels 34; Gaps 5;
21 SSSINPG-----VARGHRRGQASRRWLQGGQCECKDWFLRAPRRKFTVSG 69
183 SQSSNSGSDSKONIECVCGDKSGKHVGFCEG-----CKSFFKRSVRRN-LIYSC 236
70 LPKKQPCDHFKNVKTQRHRRKPNKHSRACQFLKQC 110
237 RGRNCPID-----QHRNQCOYCR-----LKKC 260
SULT 12
4061
pothetical protein R09A8.1 - Caenorhabditis elegans
Species: Caenorhabditis elegans
Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
Accession: T24061
Wilkinson, J.
Submitted to the EMBL Data Library, November 1995
Reference number: Z19836
Accession: T24061
Status: preliminary; translated from GB/EMBL/DDBJ
Molecule type: DNA
Residues: 1-1095 <WIL>
Cross-references: EMBL:Z58009; PIDN:CAA92003.1; GSPDB:GN00028; CESP:R09A8.1
Experimental source: clone R09A8
Genetics:
Gene: CESP:R09A8.1
Map position: X
Introns: 48/2; 189/1; 285/3; 347/3; 402/3; 482/3; 543/3; 619/1; 693/1; 771/1; 835/1; 1
Query Match 10.9%; Score 70; DB 2; Length 1095;
Best Local Similarity 31.8%; Pred. No. 29;
Matches 24; Conservative 10; Mismatches 32; Indels 10; Gaps 3;
20 VSSSLNPGVARGHRRGQASRRWLQGGQCECKDWFLRAPRRKFTVSGLPKQPCDH 79
305 VQSSSLVGGNRRSTDYRNA-ORFASTGFVEKECRWDQLVERKQ-----KKEVNSDH 355
80 FKGNVKTQRHRRK 95
356 KKAN-RITSHLENSR 370
SULT 13
7283
pothetical protein Y64G10A.f - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T27283
R:Ainscough, R.
Submitted to the EMBL Data Library, September 1999
A:Reference number: Z20336
A:Accession: T27283
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1620 <WIL>
A:Cross-references: EMBL:AL110498; NID:el542303; PIDN:CAB54471.1; CESP:Y64G10A.f
A:Experimental source: clone Y64G10A
C:Genetics:
A:Gene: CESP:Y64G10A.f
A:Introns: 77/1; 116/1; 198/1; 282/1; 365/1; 425/1; 466/1; 548/1; 559/1; 601/1; 625/1
Query Match 10.9%; Score 70; DB 2; Length 1620;
Best Local Similarity 30.0%; Pred. No. 40;
Matches 21; Conservative 10; Mismatches 35; Indels 4; Gaps 3;
QY 46 GGQCECKDWFLRAPRRKFTVSGLPKQPCDHFKGNVKTQRH--QRHRRKPNKHSRA 102
Db 261 GRAQCOQYPCFHLSDRRSCVDIDCAKNN-GCEHFCENVKTYRCKREGYQLGRDGT 319
QY 103 COQFLKOCOL 112
Db 320 CEEMUGGCQV 329
RESULT 14
C34768
ORF2 protein - Orf virus (strain NZ2)
C:Species: Orf virus
C:Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 08-Oct-1999
C:Accession: C34768
R:Fraser, K.M.; Hill, D.F.; Mercer, A.A.; Robinson, A.J.
Virology 176, 379-389, 1990
A:Title: Sequence analysis of the inverted terminal repetition in the genome of the p
A:Reference number: A34768; MUID:90266454; PMID:2129563
A:Accession: C34768
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-221 <PRA>
A:Cross-references: GB:M30023; EMBL:N37623; NID:9332561; PIDN:AAA46789.1; PID:9332565
Query Match 10.8%; Score 69.5; DB 2; Length 221;
Best Local Similarity 29.2%; Pred. No. 8.1;
Matches 33; Conservative 8; Mismatches 37; Indels 35; Gaps 6;
QY 26 PGVARGHRRGQASRRWLQGGQCECKDWFLRAPRRKFTVSGLPK-----QCP 76
Db 83 PAAARGARRRGCCARRARGGGW---RWRPRAARRG---SGPPARAPAAALAPDQAP 135
QY 77 CDHFKNVKTQR-----HQR--HHRKPNKHSRACQFLKQCQLRS 114
Db 136 ----RSKVKDLAVETLPQPTPTHTLPPARRQHRSQOACTPRRAGCSARS 184
RESULT 15
THHVB
thrombomodulin precursor [validated] - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1988 #sequence_revision 12-May-1995 #text_change 15-Sep-2000
R:Shirai, T.; Shiojiri, S.; Ito, H.; Yamamoto, S.; Kusumoto, H.; Deyashiki, Y.; Maruy
J. Biochem. 103, 281-285, 1988
A:Title: Gene structure of human thrombomodulin, a cofactor for thrombin-catalyzed ac
A:Reference number: A41442; MUID:88227901; PMID:2836377
A:Accession: A41442
A:Molecule type: DNA
A:Residues: 1-575 <SHI>
A:Cross-references: DBJ:D00210; NID:g220126; PIDN:BAA00149.1; PID:g220127
R:Jackman, R.W.; Beeler, D.L.; Fritze, L.; Soff, G.; Rosenberg, R.D.

roc. Natl. Acad. Sci. U.S.A. 84, 6425-6429, 1987
 Title: Human thrombomodulin gene is intron depleted: nucleic acid sequences of the cDN
 Reference number: A28307; MUID:87317665; PMID:2819876
 Accession: A28307
 Molecule type: DNA; mRNA
 Residues: 1-472, 'A', 474-575 <JAC>
 Cross-references: GB:J02973; NID:G339658; PIDN:AAA61175.1; PID:G339659
 Suzuki, K.; Kusumoto, H.; Deyashiki, Y.; Nishioaka, J.; Maruyama, I.; Zushi, M.; Kawaha
 480 J. 6, 1891-1897, 1987
 Title: Structure and expression of human thrombomodulin, a thrombin receptor on endoth
 Reference number: A29680; MUID:88004395; PMID:2820710
 Accession: A29680
 Molecule type: mRNA
 Residues: 1-575 <SUZ>
 Cross-references: GB:X05495; NID:G37123; PIDN:CAA29045.1; PID:G736251
 Experimental source: lung endothelium
 Note: part of this sequence, including the amino end of the mature protein, were deter
 Wen, D.; Dittman, W.A.; Ye, R.D.; Deaven, L.L.; Majerus, P.W.; Sadler, J.E.
 ochemistry 26, 4350-4357, 1987
 Title: Human thrombomodulin: complete cDNA sequence and chromosome localization of the
 Reference number: A27073; MUID:88024950; PMID:2822087
 Accession: A27073
 Molecule type: mRNA
 Residues: 1-472, 'A', 474-575 <WEN>
 Cross-references: GB:M16552; NID:G339656; PIDN:AAB59508.1; PID:G339657
 Experimental source: placenta
 Note: parts of this sequence were determined by protein sequencing
 Yamamoto, S.; Mizoquchi, T.; Tamaki, T.; Ohkuchi, M.; Kimura, S.; Aoki, N.
 Biochem 113, 433-440, 1993
 Title: Urinary thrombomodulin, its isolation and characterization.
 Reference number: JX0264; MUID:93293792; PMID:8390446
 Accession: JX0264
 Molecule type: protein; mRNA
 Residues: 19-472, 'A', 474-486 <YAM>
 Experimental source: urine
 Note: the urinary form appears to be identical with that circulating in plasma
 Gerlitz, B.; Hassell, T.; Vlahos, C.J.; Parkinson, J.F.; Bang, N.U.; Grinnell, B.W.
 ochem. J. 295, 131-140, 1993
 Title: Identification of the predominant glycosaminoglycan-attachment site in soluble
 urine.
 Reference number: S38954; MUID:94029900; PMID:8216207
 Accession: S38954
 Molecule type: protein
 Residues: 475-491, 'X', 493-494 <GER>
 Note: the residue designated 'X' was determined to be a Ser with covalently bound chor
 Meininger, D.P.; Komives, E.A.
 bmitted to the Brookhaven Protein Data Bank, September 1995
 Reference number: A57369; PDB:1ZAQ
 Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR, residue
 Tulinsky, A.; Mathews, I.I.
 bmitted to the Brookhaven Protein Data Bank, August 1994
 Reference number: A52804; PDB:1HLT
 Contents: annotation; X-ray crystallography, 3.0 angstroms, residues 426-442
 Hrabal, R.; Komives, E.A.; Ni, F.
 bmitted to the Brookhaven Protein Data Bank, November 1995
 Reference number: A65583; PDB:1FGD
 Contents: annotation; conformation by (1)H-NMR, residues 427-444
 Hrabal, R.; Komives, E.A.; Ni, F.
 otein Sci. 5, 195-203, 1996
 Title: Structural resiliency of an EGF-like subdomain bound to its target protein, the
 Reference number: A58595; MUID:96276211; PMID:8745396
 Contents: annotation; conformation by (1)H-NMR
 Genetics:
 Gene: GDB:THBD
 Cross-references: GDB:119613; OMIM:188040
 Map position: 20p11.2-20p11.2
 Introns: #status absent
 Complex: homodimer, urinary form
 Function:
 Description: inhibits thrombin activation of fibrinogen; cofactor for thrombin activat
 Pathway: blood coagulation moderation
 Note: the membrane-bound form is located on the endothelium luminal surface of arterie
 Note: thrombin complexed with the membrane-bound form is subject to endocytosis

C:Superfamily: thrombomodulin; C-type lectin homology; EGF homology
 C:Keywords: anticoagulant; beta-hydroxyasparagine; beta-hydroxyaspartic acid; blood c
 e protein
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-575/Product: thrombomodulin, membrane-bound form #status predicted <MAT>
 F:19-513/Domain: extracellular #status predicted <EXT>
 F:19-486/Product: thrombomodulin, urinary form #status experimental <MAU>
 F:24-167/Domain: C-type lectin homology <LCH>
 F:177-199/Region: PEST sequence
 F:201-233/Region: PEST sequence
 F:245-280/Domain: EGF homology <EG1>
 F:288-323/Domain: EGF homology <EG2>
 F:329-362/Domain: EGF homology <EG3>
 F:363-404/Domain: EGF homology <EG4>
 F:408-439/Domain: EGF homology <EG5>
 F:445-480/Domain: EGF homology <EG6>
 F:485-513/Region: PEST sequence
 F:517-539/Domain: transmembrane #status predicted <TMN>
 F:540-575/Domain: intracellular #status predicted <INT>
 F:47,115,116,382,409/Binding site: carbohydrate (Thr) (covalent) #status predicted
 F:174,225,411,504/Binding site: carbohydrate (Thr) (covalent) #status predicted
 F:245-256,252-265,267-280,288-296,292-308,310-323,329-340,336-349,351-362,369-378,374
 F:334,498/Binding site: carbohydrate (Ser) (covalent) #status predicted
 F:342/Modified site: erythro-beta-hydroxyasparagine (Asn) #status experimental
 F:490,492/Binding site: chondroitin sulfate (Ser) (covalent) (partial) #status experi

Query Match 10.8% Score 69.5; DB 1; Length 575;
 Best Local Similarity 23.5%; Pred. No. 18;
 Matches 24; Conservative 11; Mismatches 26; Indels 41; Gaps 5;
 QY 5 ISSLLLLPLMLMSVSSSLNPGVARGHRDRGQARRW---LQEGQECECKDFLRAPP 61
 Db 209 VGSSAAVAPLGLQLMCTAP--PGAVQGHWR-EAPGAWDCSVENGSGEHAQN----- 257
 QY 62 RKFTVSGLPKKQCP-----CDHF 80
 Db 258 ----AIPGAPRCQCPAGALQADGRCTASATOSCNLDCEHF 295

Search completed: September 13, 2003, 14:50:26
 Job time : 21.6667 secs

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4 protein - protein search, using sw model

on on: September 13, 2003, 14:32:52 ; Search time 11.3333 Seconds
(without alignments)
493.780 Million cell updates/sec

tle: US-09-786-260-1
rfect score: 644
quence: 1 MKVLISLLILLPLMLMSV.....SRACQFLKQCQLRSFALPL 119

oring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

arched: 127863 seqs, 47026705 residues

tal number of hits satisfying chosen parameters: 127863

inimum DB seq length: 0
aximum DB seq length: 2000000000

st-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

atabase : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB	ID	Description
1	77	12.0	2269	1	RRPL_SV41	P35341 simian viru
2	74.5	11.6	448	1	VDR_CHICK	P49701 coturnix co
3	74.5	11.6	451	1	VDR_CHICK	O42392 gallus gall
4	72.5	11.3	3313	1	CUR3_RAT	O88278 rattus norv
5	71	11.0	411	1	SV44_BRARE	O66725 brachydanio
6	71	11.0	1798	1	LMB2_HUMAN	P55268 homo sapien
7	71	11.0	2262	1	RRPL_P12HT	P26676 human parai
8	70	10.9	543	1	7UP1_DROME	P16375 drosophila
9	70	10.9	746	1	7UP2_DROME	P16376 drosophila
10	69.5	10.8	575	1	TEBM_HUMAN	P07204 homo sapien
11	69	10.7	314	1	SIX3_CHICK	O42406 gallus gall
12	68.5	10.6	422	1	VDR_MOUSE	P48281 mus musculus
13	68.5	10.6	422	1	VDR_XENLA	O13124 xenopus lae
14	68.5	10.6	423	1	VDR_RAT	P13053 rattus norv
15	68.5	10.6	424	1	VDR_BOVIN	O28037 bos taurus
16	68.5	10.6	427	1	VDR_HUMAN	P11473 homo sapien
17	68.5	10.6	647	1	VE1_HPV40	P36727 human papil
18	67	10.4	376	1	CEP2_ARATH	O91xw3 arabidopsis
19	67	10.4	475	1	RTM_BACSU	P42087 bacillus su
20	67	10.4	529	1	YB98_HUMAN	O9ulm2 homo sapien
21	66.5	10.3	422	1	COT1_MOUSE	O60632 mus musculus
22	66.5	10.3	423	1	COT1_HUMAN	P10589 homo sapien
23	66.5	10.3	424	1	COT1_BOVIN	O9ttr8 bos taurus
24	66.5	10.3	3301	1	CLR3_MOUSE	O91x10 mus musculus
25	66	10.2	1539	1	SNCY_HUMAN	O9bj66 homo sapien
26	65.5	10.2	646	1	VE1_HPV07	O05133 human papil
27	65.5	10.2	706	1	FZD6_HUMAN	O60953 homo sapien
28	65	10.1	363	1	PGL1_COLLN	O00446 collettotric
29	65	10.1	441	1	COAT_SCCMV	P15627 soybean chl
30	64.5	10.0	534	1	2397_HUMAN	O8nf99 homo sapien
31	64.5	10.0	622	1	MAK_MOUSE	O04859 mus musculus
32	64	9.9	227	1	N277_HUMAN	O15935 homo sapien
33	64	9.9	246	1	SIX6_CHICK	O93307 gallus gall

ALIGNMENTS

RESULT 1

```
RRPL_SV41
ID RRPL_SV41 STANDARD; PRT; 2269 AA.
AC P35341;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE RNA polymerase beta subunit (EC 2.7.7.48) (Large structural protein)
DE (L protein).
GN L
OS Simian virus 41 (SV41).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11228;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Toshiba/Chanock;
RX MEDLINE=93019033; PubMed=1328485;
RA Ogawa N., Mutsaers N., Tsurudome M., Kawano M., Matsumura H.,
RA Kusagawa S., Komada H., Nishio M., Ito Y.;
RT "Nucleotide sequence analysis of the simian virus 41 gene encoding
RT the large (L) protein and construction of a phylogenetic tree for the
RT L proteins of paramyxoviruses."
RL J. Gen. Virol. 73:2743-2750(1992).
CC -!- FUNCTION: PROBABLE COMPONENT OF THE ACTIVE POLYMERASE. IT MAY
CC FUNCTION IN MRNA SYNTHESIS, CAPPING, METHYLATION AND POLY(A)
CC SYNTHESIS OF NEWLY SYNTHESIZED VIRAL MRNAs, RNA EDITING OF THE P
CC GENE TRANSCRIPT, AND PROTEIN KINASE ACTIVITY.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC [RNA](N).
CC -!- SIMILARITY: WITH L PROTEIN OF OTHER PARAMYXOVIRUSES.
CC -----
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X64275; CAA45569.1;
CC PIR: JQ1750; JQ1750.
CC InterPro: IPR007098; RNA_pol_monon.
CC InterPro: IPR001016; Viral_RNA_pol.L.
CC Pfam: PF00946; Paramyx_RNA_pol; 1.
CC Transferrase; RNA-directed RNA polymerase.
CC SEQUENCE 2269 AA; 256429 MW; 3BD50C14AA161F5B CRC64;
```

Query Match 12.0%; Score 77; DB 1; Length 2269;
Best Local Similarity 27.5%; Pred. No. 47;
Matches 30; Conservative 12; Mismatches 31; Indels 36; Gaps 6;
QY 13 PLMLMSVSSSLNPGVARGHRDQGAS-----RRWLQ-----EGGOCE--CK 53
DB 422 PLSLPGNASKSL-----TELHDNSEISYEYTLRWKLSLIEFKKCFDPPGELSIFMK 477

54 DWFLAPRRKEMTVSGLPKKQPCDHFKNVKKTRHORHH-RKPNKHSR 101
 478 DKAISAPKEDWMSV-----FRKSLIKQRHQRHHIPMPNPNR 514

SULT 2

R_COTJJA STANDARD; PRT; 448 AA.
 P49701:
 01-FEB-1996 (Rel. 33, Created)
 01-FEB-1996 (Rel. 33, Last sequence update)
 28-FEB-2003 (Rel. 41, Last annotation update)
 Vitamin D3 receptor (VDR) (1,25-dihydroxyvitamin D3 receptor).
 VDR OR NR11.
 Coturnix coturnix japonica (Japanese quail).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Coturnix.
 NCBI_TaxID=93934;
 [1]
 SEQUENCE FROM N.A. (ISOFORMS A AND B).
 TISSUE=Choricoallantoic membrane;
 MEDLINE=95062315; PubMed=7972109;
 Eiaroussi M.A., Prahil J.M., Deluca H.F.;
 "The avian vitamin D receptors: primary structures and their
 origins";
 Proc. Natl. Acad. Sci. U.S.A. 91:11596-11600(1994).
 -!- FUNCTION: VDR MEDIATES THE ACTION OF VITAMIN D3 BY CONTROLLING THE
 EXPRESSION OF HORMONE SENSITIVE GENES.
 -!- SUBCELLULAR LOCATION: Nuclear.
 -!- ALTERNATIVE PRODUCTS:
 Event-Alternative initiation;
 Comment=2 isoforms, A (shown here) and B, are produced by
 alternative initiation;
 -!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
 A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
 -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NRI
 subfamily.

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EMBL; U12641; AAA56725.1; -;
 PIR; I50451; I50451.
 HSSP; O75469; IILG.
 InterPro; IPR000536; Hormone_rec_lig.
 InterPro; IPR001723; Stdhrmn_receptor.
 InterPro; IPR001628; Znf_C4steroid.
 Pfam; PF00104; hormone_rec; 1.
 Pfam; PF00105; zf-C4; 1.
 PRINTS; PR00398; STRDHORMONER.
 PRINTS; PR00047; STROIDFINGER.
 ProDom; PD000035; Znf_C4steroid; 1.
 SMART; SM00430; HOL1; 1.
 SMART; SM00399; Znf_C4; 1.
 PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
 Receptor; Transcription regulation; DNA-binding; Nuclear protein;
 Zinc-finger; Alternative initiation.
 CHAIN 1 448 VITAMIN D3 RECEPTOR, ISOFORM A.
 VITAMIN D3 RECEPTOR, ISOFORM B.
 INIT_MET 26 26 FOR ISOFORM B.
 DNA_BIND 44 109 NUCLEAR RECEPTOR-TYPE.
 2N_FING 44 64 C4-TYPE.
 ZN_FING 80 104 C4-TYPE.
 DOMAIN 110 212 HINGE.
 DOMAIN 213 448 LIGAND-BINDING.
 SEQUENCE 448 AA; 50668 MW; FCFIFC3DEAEAF3E CRC64;

Query Match 11.6%; Score 74.5; DB 1; Length 448;
 Best Local Similarity 32.9%; Pred. No. 1.8;
 Matches 24; Conservative 11; Mismatches 15; Indels 23; Gaps 6;
 QY 50 CE-CKDNFLAPRRKEMTVSGLPKKQPCDHFKNVKKTRHORHH-RKPNKHSRACQOFLK 108
 DB 61 CEGCKGFFRRSKRKAMFT-----CP---FSGCKITKDNR-----RHCQACR--LK 102

QY 109 QC-----QLRSFAL 117

DB 103 RCVDICGMKEFIL 115

RESULT 3

VDR_CHICK STANDARD; PRT; 451 AA.
 ID VDR_CHICK
 AC O42392;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 23-FEB-2003 (Rel. 41, Last annotation update)
 DE Vitamin D3 receptor (VDR) (1,25-dihydroxyvitamin D3 receptor).
 GN VDR OR NR11.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 OC Gallus.
 NCBI_TaxID=9031;
 RN NCBI_TaxID=9031;
 RN [1]
 SEQUENCE FROM N.A. (ISOFORMS A AND B).
 PC STRAIN=Leghorn; TISSUE=Kidney;
 RX MEDLINE=97223369; PubMed=9056239;
 RA Lu Z., Hanson K., Deluca H.F.;
 RT "Cloning and origin of the two forms of chicken vitamin D receptor.";
 RL Arch. Biochem. Biophys. 339:99-106(1997).
 RN [2]
 RN SEQUENCE OF 45-114 FROM N.A.
 RP MEDLINE=87149040; PubMed=3029866;
 RA McDonnell D.P., Mangelsdorf D.J., Pike J.W., Haussler M.R.,
 O'Malley B.W.;
 RT "Molecular cloning of complementary DNA encoding the avian receptor
 for vitamin D.";
 RL Science 235:1214-1217(1987).
 CC -!- FUNCTION: VDR MEDIATES THE ACTION OF VITAMIN D3 BY CONTROLLING THE
 EXPRESSION OF HORMONE SENSITIVE GENES.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- ALTERNATIVE PRODUCTS:
 Event-Alternative initiation;
 Comment=2 isoforms, A (shown here) and B, are produced by
 alternative initiation;
 -!- TISSUE SPECIFICITY: EXPRESSED IN KIDNEY AND INTESTINE.
 -!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
 A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
 CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NRI
 subfamily.

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 or send an email to license@isb-sib.ch).

EMBL; AF011356; AAB62579.1; -;

PIR; A60912; A60912.

HSSP; O75469; IILG.

TRANSFAC; T00884; -;

InterPro; IPR000536; Hormone_rec_lig.

InterPro; IPR001723; Stdhrmn_receptor.

InterPro; IPR001628; Znf_C4steroid.

Pfam; PF00104; hormone_rec; 1.

Pfam; PF00105; zf-C4; 1.

PRINTS; PR00398; STRDHORMONER.


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PRINTS: PR00047; STROIDFINGER.
PRODOM; PD000035; Znf_C4steroid; 1.
SMART; SM00430; HOLI; 1.
SMART; SM00399; Znf_C4; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
Receptor; Transcription regulation; DNA-binding; Nuclear protein;
Zinc-finger; Alternative initiation.
CHAIN 1 451 VITAMIN D3 RECEPTOR, ISOFORM A.
INIT_MET 15 451 VITAMIN D3 RECEPTOR, ISOFORM B.
NUCLEO_BIND 47 112 FOR ISOFORM B.
NUCLEO_BIND 47 112 NUCLEAR RECEPTOR-TYPE.
ZN_FING 47 67 C4-TYPE.
ZN_FING 83 107 C4-TYPE.
DOMAIN 113 215 HINGE.
DOMAIN 216 451 LIGAND-BINDING.
SEQUENCE 451 AA; 51299 MW; 207986A6C8D8E5FC CRC64;

Query Match 11.6%; Score 74.5; DB 1; Length 451;
Best Local Similarity 32.9%; Pred. No. 1.8;
Matches 24; Conservative 11; Mismatches 15; Indels 23; Gaps 6;

50 CE-CKDWFLAPRRKWTWSSGLPKKPCDHPKGNVKKTRHORHHRKPNKHSRACQQLK 108
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
64 CEGCKGFRRSMRKAMFT-----CP---FNGCKITKDN-----RHQACR--LK 105

109 QC-----QLRSFAL 117
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
106 RCVDIGMKKEFIL 118

SEQUENCE FROM N.A.
STRAIN-Sprague-Dawley; TISSUE-Brain;
MEDLINE-98360089; PubMed-9693030;
Nakayama M., Nakajima D., Nagase T., Nomura N., Seki N., Ohara O.;
"Identification of high-molecular-weight proteins with multiple
EGF-like motifs by motif-trap screening.";
Genomics 51:27-34(1998).
-!- FUNCTION: Receptor that may have an important role in cell/cell
signaling during nervous system formation.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: Expressed in the brain. Expressed in
cerebellum, olfactory bulb, cerebral cortex, hippocampus and
brain stem.
-!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
-!- SIMILARITY: Contains 9 cadherin domains.
-!- SIMILARITY: Contains 8 EGF-like domains.
-!- SIMILARITY: Contains 2 laminin G-like domains.
-!- SIMILARITY: Contains 1 laminin EGF-like domain.
-!- SIMILARITY: Contains 1 GPS domain.

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EMBL; AB011528; BAA32459.1; -.
DR HSP; P00740; 1EDM.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR002136; Cadherin.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR000203; PKD_cys_rich.
DR Pfam; PF00002; 7tm2_1.
DR Pfam; PF00028; cadherin; 9.
DR Pfam; PF00008; EGF; 6.
DR Pfam; PF01825; GPS; 1.
DR Pfam; PF02793; HRM; 1.
DR Pfam; PF00054; laminin_G; 1.
DR PRINTS; PR00205; CADHERIN.
DR PRINTS; PR00011; EGFLAMININ.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00112; CA; 9.
DR SMART; SM00181; EGF; 6.
DR SMART; SM00303; GPS; 1.
DR SMART; SM00008; HORM; 1.
DR SMART; SM0282; LANG; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00232; CADHERIN_1; 7.
DR PROSITE; PS00288; CADHERIN_2; 8.
DR PROSITE; PS00022; EGF_1; 6.
DR PROSITE; PS01186; EGF_2; 4.
DR PROSITE; PS00221; GPS; 1.
DR PROSITE; PS00025; LAM_G_DOMAIN; 2.
DR PROSITE; PS00649; G_PROTEIN_RECP_F2_1; FALSE_NEG.
DR PROSITE; PS00650; G_PROTEIN_RECP_F2_2; FALSE_NEG.
DR PROSITE; PS00227; G_PROTEIN_RECP_F2_3; 1.
DR PROSITE; PS00261; G_PROTEIN_RECP_F2_4; 1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW EGF-like domain; Calcium-binding; Laminin EGF-like domain; Repeat;
KW Developmental protein; Signal; Hydroxylation; Signal.
FT SIGNAL 1 31 POTENTIAL.
FT CHAIN 32 3313 CADHERIN EGF LAG SEVEN-PASS G-TYPE
RECEPTOR 3
EXTRACELLULAR (POTENTIAL).
1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CADHERIN 1.
CADHERIN 2.
CADHERIN 3.
CADHERIN 4.
CADHERIN 5.
CADHERIN 6.
CADHERIN 7.
CADHERIN 8.
CADHERIN 9.
EGF-LIKE 1. CALCIUM-BINDING.
EGF-LIKE 2. CALCIUM-BINDING.
EGF-LIKE 3. CALCIUM-BINDING.
LAMININ G-LIKE 1.
1710
```

DOMAIN 1713 1749 EGF-LIKE 4, CALCIUM-BINDING.
 DOMAIN 1753 1935 LAMININ G-LIKE 2.
 DOMAIN 1937 1972 EGF-LIKE 5, CALCIUM-BINDING.
 DOMAIN 1973 2011 EGF-LIKE 6, CALCIUM-BINDING.
 DOMAIN 2012 2044 EGF-LIKE 7, CALCIUM-BINDING.
 DOMAIN 2046 2081 EGF-LIKE 8, CALCIUM-BINDING.
 DOMAIN 2087 2120 LAMININ EGF-LIKE.
 DOMAIN 2120 2527 GPS.
 DOMAIN 2475 2527 BY SIMILARITY.
 DISULFID 1370 1381 BY SIMILARITY.
 DISULFID 1375 1412 BY SIMILARITY.
 DISULFID 1414 1423 BY SIMILARITY.
 DISULFID 1430 1441 BY SIMILARITY.
 DISULFID 1450 1461 BY SIMILARITY.
 DISULFID 1452 1461 BY SIMILARITY.
 DISULFID 1470 1481 BY SIMILARITY.
 DISULFID 1475 1491 BY SIMILARITY.
 DISULFID 1493 1504 BY SIMILARITY.
 DISULFID 1717 1728 BY SIMILARITY.
 DISULFID 1722 1737 BY SIMILARITY.
 DISULFID 1739 1748 BY SIMILARITY.
 DISULFID 1941 1952 BY SIMILARITY.
 DISULFID 1946 1961 BY SIMILARITY.
 DISULFID 1963 1972 BY SIMILARITY.
 DISULFID 1976 1987 BY SIMILARITY.
 DISULFID 1981 1999 BY SIMILARITY.
 DISULFID 2001 2010 BY SIMILARITY.
 DISULFID 2018 2031 BY SIMILARITY.
 DISULFID 2033 2043 BY SIMILARITY.
 DISULFID 2050 2065 BY SIMILARITY.
 DISULFID 2052 2068 BY SIMILARITY.
 DISULFID 2070 2080 BY SIMILARITY.
 MOD_RES 1954 1954 HYDROXYLATION (POTENTIAL).
 CARBOHYD 623 623 N-LINKED (GLCNAC. .) (POTENTIAL).
 CARBOHYD 838 838 N-LINKED (GLCNAC. .) (POTENTIAL).
 CARBOHYD 1173 1173 N-LINKED (GLCNAC. .) (POTENTIAL).
 CARBOHYD 1213 1213 N-LINKED (GLCNAC. .) (POTENTIAL).
 CARBOHYD 1308 1308 N-LINKED (GLCNAC. .) (POTENTIAL).
 CARBOHYD 1318 1318 N-LINKED (GLCNAC. .) (POTENTIAL).
 CARBOHYD 1640 1640 N-LINKED (GLCNAC. .) (POTENTIAL).
 CARBOHYD 1704 1704 N-LINKED (GLCNAC. .) (POTENTIAL).
 CARBOHYD 1761 1761 N-LINKED (GLCNAC. .) (POTENTIAL).
 CARBOHYD 2044 2044 N-LINKED (GLCNAC. .) (POTENTIAL).
 CARBOHYD 2173 2173 N-LINKED (GLCNAC. .) (POTENTIAL).
 CARBOHYD 2192 2192 N-LINKED (GLCNAC. .) (POTENTIAL).
 CARBOHYD 2382 2382 N-LINKED (GLCNAC. .) (POTENTIAL).
 CARBOHYD 2472 2472 N-LINKED (GLCNAC. .) (POTENTIAL).
 CARBOHYD 2504 2504 N-LINKED (GLCNAC. .) (POTENTIAL).
 SEQUENCE 3313 AA; 559348 MW; 511DA09517288764 CRC64;

Query Match 11.3%; Score 72.5; DB 1; Length 3313;
 Best Local Similarity 27.6%; Pred. No. 20;
 Matches 35; Conservative 9; Mismatches 40; Indels 43; Gaps 7;

24 LNPVGARGHRDGOASRWLEQ--GQCECKDWFL-----RAPRRKFTVSGLP 71
 1778 LNP-----CQNGGCRHLQGGPHGTCDGASGYFGQHCHEHMDQCQPRGHWGSGTGP 2030
 72 KQCPDHPKRG---NVKTKRHRH-----HRKP-----NKHSRACQOFLKQC 110
 2031 ---CNCVDHKGDPNCKTSGQCHCKEFHVRPRGSDCLPCDYPVGSSTRSCAPHSGQC 2087
 111 QLRSFAL 117
 2088 PCRPGL 2094

SULT 5
 44_BRAE STANDARD; PRT; 411 AA.
 SV44_BRAE
 Q06725;
 15-JUL-1999 (Rel. 36, Created)
 15-JUL-1999 (Rel. 38, Last sequence update)
 28-FEB-2003 (Rel. 41, Last annotation update)

DE Steroid receptor homolog SVP 44.
 GN SVP44 OR NR2F1.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93223680; PubMed=8467797;
 RA FJosa A., Norries S., Weber U., Mlodzik M.;
 RT "Functional conservation of vertebrate seven-up related genes in
 RT neurogenesis and eye development.";
 RL EMBO J. 12:1403-1414(1993).
 CC -1- FUNCTION: PUTATIVE RECEPTOR THAT IS REQUIRED IN PHOTORECEPTOR
 CC CELLS PRECURSORS DURING EYE DEVELOPMENT.
 CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -1- SIMILARITY: Belongs to the nuclear hormone receptor family. NR2
 CC subfamily.
 CC -----
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 CC -----
 DR EMBL; X70299; CAA49780.1; -;
 DR PIR; S35333; S35333.
 DR HSP; P19793; 2NLL.
 DR ZFIN; ZDB-GENE-980526-115; nr2f1.
 DR InterPro; IPR000536; Hormone_rec_lig.
 DR InterPro; IPR001723; Stdhrmn_receptor.
 DR InterPro; IPR001628; znf_C4steroid.
 DR Pfam; PF00104; hormone_rec; 1.
 DR Pfam; PF00105; zf-C4; 1.
 DR PRINTS; PR00398; STRDHORMONER.
 DR PRINTS; PR00047; STROIDFINGER.
 DR ProDom; PD000035; znf_C4steroid; 1.
 DR SMART; SM00430; HOL1; 1.
 DR SMART; SM00399; znf_C4; 1.
 DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
 DR Receptor; Transcription regulation; DNA-binding; Nuclear protein;
 DR Zinc-finger; Vision.
 FT DNA_BIND 76 141 NUCLEAR RECEPTOR-TYPE.
 FT ZN_FING 76 96 C4-TYPE.
 FT ZN_FING 112 136 C4-TYPE.
 FT SEQUENCE 411 AA; 45482 MW; B0405FB4EFA0202 CRC64;
 SQ

Query Match 11.0%; Score 71; DB 1; Length 411;
 Best Local Similarity 26.3%; Pred. No. 3.8;
 Matches 26; Conservative 14; Mismatches 27; Indels 32; Gaps 6;

QY 26 PGVA--RGHRDGOASRR-----WLOGGQCE-CKDWFLRAPRRKFTVSGLP 71
 DB 56 PGTAGDKGSGNSGQSQHIECVGDKSGSKHYGFTGCGCKSFKRSVRN-LTYTCRA 114
 QY 72 KQCPDHPKRGVKNKTRHQRHHRKPNKHSRACQOFLKQC 110
 DB 115 NRNCPID-----QHRNQCQYCR-----LKKC 136

RESULT 6
 LMB2_HUMAN STANDARD; PRT; 1798 AA.
 ID AC P52268; Q16321;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Laminin beta-2 chain precursor (S-laminin) (laminin B1s chain).
 GN LMB2 OR LAMS.
 OS Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
MEDLINE=95213013; PubMed=7698745;
Wewer U.M., Gerecke D.R., Durkin M.E., Kurtz K.S., Mattei M.-G., Champlaud M.F., Burgess R.E., Abrechtsen R.;
"Human beta 2 chain of laminin (formerly S chain): cDNA cloning, chromosomal localization, and expression in carcinomas";
Genomics 24:243-252(1994).
[2]
SEQUENCE FROM N.A.
MEDLINE=95316263; PubMed=7795887;
Iivanainen A., Vuolteenaho R., Sainio K., Eddy R., Shows T.B., Sariola H., Tryggvason K.;
"The human laminin beta 2 chain (S-laminin): structure, expression in fetal tissues and chromosomal assignment of the LAMB2 gene";
Matrix Biol. 14:489-497(1995).
-!- FUNCTION: Binding to cells via a high affinity receptor, laminin is thought to mediate the attachment, migration, and organization of cells into tissues during embryonic development by interacting with other extracellular matrix components.
-!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three different polypeptide chains (alpha, beta, gamma), which are bound to each other by disulfide bonds into a cross-shaped molecule comprising one long and three short arms with globules at each end.
THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4 (S-MEROSIN), AND LAMININ-7 (KS-LAMININ).
-!- SUBCELLULAR LOCATION: Extracellular.
-!- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR COMPONENT). S-LAMININ IS CONCENTRATED IN THE SYNAPTIC CLEFT OF THE NEUROMUSCULAR JUNCTION.
-!- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
-!- DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.
-!- SIMILARITY: Contains 1 laminin N-terminal domain.
-!- SIMILARITY: Contains 13 laminin EGF-like domains.
-!- SIMILARITY: Contains 1 laminin IV domain.

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EMBL; 268155; CAA92279.1; -
EMBL; 268156; CAA92279.1; JOINED.
EMBL; X79683; CAA56130.1; -
EMBL; S77512; AAB34692.2; -
PIR; S53869; S53869.
HSP; P02468; IKLO.
Genew; HGNC:6487; LAMB2.
MIM; 150325; -
GO; GO:0005605; C-basal lamina; TAS.
InterPro; IPR006209; EGF-like.
InterPro; IPR002049; Laminin_EGF.
InterPro; IPR001886; LamNT.
Pfam; PF00053; laminin_EGF; 13.
Pfam; PF00055; laminin_Nterm; 1.
PRINTS; PR00011; EGF_LAMININ.
SMART; SM00180; EGF_Lam; 13.
SMART; SM00136; LamNT; 1.
PROSITE; PS00022; EGF_1; 10.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01248; LAMININ_TYPE_EGF; 12.
Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
SIGNAL 1 32 POTENTIAL.
CHAIN 33 1798 LAMININ BETA-2 CHAIN.

FT DOMAIN 33 280 LAMININ N-TERMINAL (DOMAIN VI).
FT DOMAIN 283 346 LAMININ EGF-LIKE 1.
FT DOMAIN 347 409 LAMININ EGF-LIKE 2.
FT DOMAIN 410 469 LAMININ EGF-LIKE 3.
FT DOMAIN 470 521 LAMININ EGF-LIKE 4.
FT DOMAIN 522 552 LAMININ EGF-LIKE 5 (INCOMPLETE).
FT DOMAIN 553 781 LAMININ DOMAIN IV.
FT DOMAIN 783 830 LAMININ EGF-LIKE 6.
FT DOMAIN 831 876 LAMININ EGF-LIKE 7.
FT DOMAIN 877 926 LAMININ EGF-LIKE 8.
FT DOMAIN 927 985 LAMININ EGF-LIKE 9.
FT DOMAIN 986 1037 LAMININ EGF-LIKE 10.
FT DOMAIN 1038 1094 LAMININ EGF-LIKE 11.
FT DOMAIN 1095 1142 LAMININ EGF-LIKE 12.
FT DOMAIN 1143 1189 LAMININ EGF-LIKE 13.
FT DOMAIN 1190 1409 DOMAIN II.
FT DOMAIN 1410 1442 DOMAIN I.
FT DOMAIN 1443 1798 COILED COIL (POTENTIAL).
FT DOMAIN 1799 1830 COILED COIL (POTENTIAL).
FT DISULFID 283 292 BY SIMILARITY.
FT DISULFID 285 310 BY SIMILARITY.
FT DISULFID 312 321 BY SIMILARITY.
FT DISULFID 324 344 BY SIMILARITY.
FT DISULFID 347 356 BY SIMILARITY.
FT DISULFID 349 374 BY SIMILARITY.
FT DISULFID 377 386 BY SIMILARITY.
FT DISULFID 389 407 BY SIMILARITY.
FT DISULFID 410 423 BY SIMILARITY.
FT DISULFID 412 438 BY SIMILARITY.
FT DISULFID 440 449 BY SIMILARITY.
FT DISULFID 452 467 BY SIMILARITY.
FT DISULFID 470 484 BY SIMILARITY.
FT DISULFID 472 491 BY SIMILARITY.
FT DISULFID 493 502 BY SIMILARITY.
FT DISULFID 505 519 BY SIMILARITY.
FT DISULFID 783 795 BY SIMILARITY.
FT DISULFID 785 802 BY SIMILARITY.
FT DISULFID 804 813 BY SIMILARITY.
FT DISULFID 816 828 BY SIMILARITY.
FT DISULFID 831 843 BY SIMILARITY.
FT DISULFID 833 850 BY SIMILARITY.
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FT DISULFID 864 874 BY SIMILARITY.
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FT DISULFID 927 943 BY SIMILARITY.
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FT DISULFID 1095 1107 BY SIMILARITY.
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FT DISULFID 1116 1125 BY SIMILARITY.
FT DISULFID 1128 1140 BY SIMILARITY.
FT DISULFID 1143 1155 BY SIMILARITY.
FT DISULFID 1145 1162 BY SIMILARITY.
FT DISULFID 1164 1173 BY SIMILARITY.
FT DISULFID 1176 1187 BY SIMILARITY.
FT DISULFID 1190 1190 INTERCHAIN (PROBABLE).
FT DISULFID 1193 1193 INTERCHAIN (PROBABLE).
FT DISULFID 1797 1797 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 248 248 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 368 368 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1085 1085 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1249 1249 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1308 1308 N-LINKED (GLCNAC. . .) (POTENTIAL).


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70 LFAAQCPCDGRFQWVAKIRNQAHKARAFNRASGQQEINQC 110
      :| | | :| | | :| | |
237 RGSRCNPID-----QHRRNQCQYCR-----LKKC 260

RESULT 10
TREMB_HUMAN
ID TREMB_HUMAN STANDARD; PRT; 575 AA.
AC P07204;
DT 01-APR-1988 (Rel. 07, Created)
DI 01-FEB-1991 (Rel. 17, Last sequence update)
DDT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Thrombosmodulin precursor (Fetomodulin) (TM) (CD141 antigen).
GN THBD OR THRBM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]

```

- SEQUENCE FROM N.A.
MEDLINE=98004395; PubMed=2820710;
Suzuki K., Kusumoto H., Deyashiki Y., Nishioka J., Maruyama I.,
Zushi M., Kawahara S., Honda G., Yamamoto S., Horiguchi S.;
"Structure and expression of human thrombomodulin, a thrombin
receptor on endothelium acting as a cofactor for protein C
activation.";
EMBO J. 6:1891-1897(1987).
[2]
SEQUENCE FROM N.A.
MEDLINE=88024950; PubMed=2822087;
Wen D., Dittman W.A., Ye R.D., Deaven L.L., Majerus P.W., Sadler J.E.;
"Human thrombomodulin: complete cDNA sequence and chromosome
localization of the gene.";
Biochemistry 26:4350-4357(1987).
[3]
SEQUENCE FROM N.A.
MEDLINE=87317685; PubMed=2819876;
Jackman R.W., Beeler D.L., Fritze L., Soff G., Rosenberg R.D.;
"Human thrombomodulin gene is intron depleted: nucleic acid sequences
of the cDNA and gene predict protein structure and suggest sites of
regulatory control.";
Proc. Natl. Acad. Sci. U.S.A. 84:6425-6429(1987).
[4]
SEQUENCE FROM N.A.
MEDLINE=88227901; PubMed=2836377;
Shirai T., Shiojiri S., Ito H., Yamamoto S., Kusumoto H.,
Deyashiki Y., Maruyama I., Suzuki K.;
"Gene structure of human thrombomodulin, a cofactor for thrombin-
catalyzed activation of protein C.";
J. Biochem. 103:281-285(1988).
[5]
SEQUENCE FROM N.A.
Rieder M.J., Armel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
Ozuna M., Peel C.L., Toth E.J., Yi Q., Nickerson D.A.;
Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
[6]
SEQUENCE FROM N.A.
MEDLINE=21638749; PubMed=11780052;
Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L.,
Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.V., Clee C.M.,
Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
Graffham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
Lehvaeslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
Marsh V.L., Martin S.B., McConachie L.J., McLeay K., McMurray A.A.,
Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
Olivier K., Parker A., Pearce T.A.V., Peck A.I.,
Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,
Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
Rogers J.;
"The DNA sequence and comparative analysis of human chromosome 20.";
Nature 414:865-871(2001).
[7]
CARBOHYDRATE-LINKAGE SITE SER-492, AND MUTAGENESIS.
MEDLINE=94029900; PubMed=8216207;
Gerleitz B., Hassell T., Vlahos C.J., Parkinson J.F., Bang N.U.,
Grinnell B.W.;
"Identification of the predominant glycosaminoglycan-attachment site
in soluble recombinant human thrombomodulin: potential regulation of
- RT functionality by glycosyltransferase competition for serine474.";
Biochem. J. 295:131-140(1993).
[8]
RT STRUCTURE BY NMR OF 389-407.
RX MEDLINE=96007474; PubMed=7559494;
RX Adler M., Seto M.H., Nitecki D.E., Lin J.H., Light D.R., Morser J.;
"The structure of a 19-residue fragment from the C-loop of the fourth
epidermal growth factor-like domain of thrombomodulin.";
J. Biol. Chem. 270:23366-23372(1995).
[9]
RT STRUCTURE BY NMR OF 364-407.
RX MEDLINE=96100636; PubMed=8528067;
RX Meininger D.P., Hunter M.J., Komives E.A.;
"Synthesis, activity, and preliminary structure of the fourth
EGF-like domain of thrombomodulin.";
Protein Sci. 4:1683-1695(1995).
[10]
RT STRUCTURE BY NMR OF 427-444.
RX MEDLINE=95034791; PubMed=7947766;
RX Srinivasan J., Hu S., Hrabal R., Zhu Y., Komives E.A., Ni F.;
"Thrombin-bound structure of an EGF subdomain from human
thrombomodulin determined by transferred nuclear Overhauser
effects.";
Biochemistry 33:13553-13560(1994).
[11]
RT STRUCTURE BY NMR OF 427-444.
RX MEDLINE=96276211; PubMed=8745396;
RX Hrabal R., Komives E.A., Ni F.;
"Structural resiliency of an EGF-like subdomain bound to its target
protein, thrombin.";
Protein Sci. 5:195-203(1996).
[12]
RT STRUCTURE BY NMR OF 405-444.
RX MEDLINE=98035729; PubMed=9367781;
RX Sampoli Benitez B.A., Hunter M.J., Meininger D.P., Komives E.A.;
"Structure of the fifth EGF-like domain of thrombomodulin: an
EGF-like domain with a novel disulfide-bonding pattern.";
J. Mol. Biol. 273:913-926(1997).
[13]
RT VARIANT TED TYR-486.
RX MEDLINE=95111115; PubMed=7811989;
RX Oehlén A.-K., Marlar R.A.;
"The first mutation identified in the thrombomodulin gene in a
45-year-old man presenting with thromboembolic disease.";
Blood 85:330-336(1995).
[14]
RT VARIANT TED TYR-486, AND VARIANTS THR-43; ALA-79; SER-495 AND LEU-501.
RX MEDLINE=97341986; PubMed=9198186;
RX Oehlén A.-K., Norlund L., Marlar R.A.;
"Thrombomodulin gene variations and thromboembolic disease.";
Thromb. Haemost. 78:396-400(1997).
[15]
RT VARIANT VAL-473.
RX MEDLINE=97206518; PubMed=9157575;
RX Norlund L., Holm J., Zoller B., Oehlén A.-K.;
"A common thrombomodulin amino acid dimorphism is associated with
myocardial infarction.";
Thromb. Haemost. 77:248-251(1997).
[16]
RT VARIANT THR-43.
RX MEDLINE=99057299; PubMed=9843165;
RX Doggen C.J.M., Kunz G., Rosendaal F.R., Lane D.A., Vos H.L.,
Stubbs P.J., Manger Cats V., Ireland H.;
"A mutation in the thrombomodulin gene, 127G to A coding for Ala25Thr,
and the risk of myocardial infarction in men.";
Thromb. Haemost. 80:743-748(1998).
[17]
RT VARIANT VAL-473.
RX MEDLINE=21143723; PubMed=11245641;
RX Wu K.K., Aleksic N., Ahn C., Boerwinkle E., Folsom A.R.,
Juneja H.;
"Thrombomodulin Ala455Val polymorphism and risk of coronary heart
disease.";


```

-!- SUBCELLULAR LOCATION: Nuclear.
-!- DOMAIN: Composed of three domains: a modulating N-terminal domain,
a DNA-binding domain and a C-terminal steroid-binding domain.
-!- SIMILARITY: Belongs to the nuclear hormone receptor family. NRI
subfamily.

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or send an email to licensed@isb-sib.ch).
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EMBL; D31969; BAA06737.1; .
PIR; PC4019; PC4019.
HSSP; P03372; HSCQ.
TRANSFAC; T00883; .
MGD; MGI:103076; Vdr.
GO; GO:0006874; P:calcium ion homeostasis; IMP.
GO; GO:0007275; P:development; IMP.
GO; GO:0001501; P:skeletal development; IMP.
InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001723; Stdhrmn_receptor.
InterPro; IPR001628; Znf_C4steroid.
Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zif-C4; 1.
PRINTS; PR00398; STRDHORMNER.
PROSITE; PR00047; STROIDFINGER.
ProDom; PD000035; Znf_C4steroid; 1.
SMART; SM00430; HOLI; 1.
SMART; SM00399; ZNF_C4; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
Receptor; Transcription regulation; DNA-binding; Nuclear protein;
Zinc-finger; Phosphorylation.
DNA_BIND 24 89 NUCLEAR RECEPTOR-TYPE.
ZNF_FING 24 89 C4-TYPE.
ZNF_FING 60 84 C4-TYPE.
DOMAIN 90 186 HINGE.
DOMAIN 187 422 LIGAND-BINDING.
SEQUENCE 422 AA; 47851 MW; 4704CC8172445732 CRC64;

Query Match 10.6%; Score 68.5; DB 1; Length 422;
Best Local Similarity 30.1%; Pred. No. 7.2;
Matches 22; Conservative 13; Mismatches 15; Indels 23; Gaps 6;

50 CE-CKDWFLRPRKFTVSGLPKQPCDHFHKGNYKTRHQRHHRKPNKHSRACQQLK 108
41 CEGCKGFFRSMKRKALFT-----CP---FNGDCRITKDNR-----RHQACR--LK 82

109 QC-----QLRSFAL 117
83 RCVDIGMKKEFIL 95

VDR_XENLA STANDARD; PRT; 422 AA.
O13124;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUL-1999 (Rel. 39, Last annotation update)
Vitamin D3 receptor (VDR) (1,25-dihydroxyvitamin D3 receptor).
VDR OR NR1I1.
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodinae; Xenopus.
NCBI_TaxID=8355;
[1]
SEQUENCE FROM N.A.
TISSUE=Kidney;
MEDLINE=97307679; PubMed=9165021;

```

```

RA Li Y.C., Bergwitz C., Jueppner H., Demay M.B.;
RT "Cloning and characterization of the vitamin D receptor from Xenopus
RL laevis.";
CC Endocrinology 138:2347-2353(1997).
CC -!- FUNCTION: VDR MEDIATES THE ACTION OF VITAMIN D3 BY CONTROLLING
CC THE EXPRESSION OF HORMONE SENSITIVE GENES.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: DETECTED IN ALL THE TISSUE EXAMINED. HIGHEST
CC LEVEL IN SMALL INTESTINE AND SKIN.
CC -!- DEVELOPMENTAL STAGE: FIRST DETECTED AT STAGE 13. INCREASES
CC GRADUALLY AND PEAKS AT STAGE 57-61 THEN DECREASES TO THE LEVEL
CC SEEN IN ADULT.
CC -!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NRI
CC subfamily.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to licensed@isb-sib.ch).
CC -----
CC EMBL; U91846; AAB58585.1; .
CC HSSP; O75469; ILIG.
CC InterPro; IPR000536; Hormone_rec_lig.
CC InterPro; IPR001723; Stdhrmn_receptor.
CC InterPro; IPR001628; Znf_C4steroid.
CC Pfam; PF00104; hormone_rec; 1.
CC Pfam; PF00105; zif-C4; 1.
CC PRINTS; PR00398; STRDHORMNER.
CC PRINTS; PR00047; STROIDFINGER.
CC ProDom; PD000035; Znf_C4steroid; 1.
CC SMART; SM00430; HOLI; 1.
CC SMART; SM00399; ZNF_C4; 1.
CC PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
KW Zinc-finger.
FT DNF_BIND 25 90 NUCLEAR RECEPTOR-TYPE.
FT ZNF_FING 25 45 C4-TYPE.
FT ZNF_FING 61 85 C4-TYPE.
FT DOMAIN 91 188 HINGE.
FT DOMAIN 189 422 LIGAND-BINDING.
FT SEQUENCE 422 AA; 48188 MW; C8A9F25414FEE9D5 CRC64;

Query Match 10.6%; Score 68.5; DB 1; Length 422;
Best Local Similarity 30.1%; Pred. No. 7.2;
Matches 22; Conservative 13; Mismatches 15; Indels 23; Gaps 6;

50 CE-CKDWFLRPRKFTVSGLPKQPCDHFHKGNYKTRHQRHHRKPNKHSRACQQLK 108
42 CEGCKGFFRSMKRKAMFT-----CP---FNGDCRITKDNR-----RHQACR--LK 83

109 QC-----QLRSFAL 117
84 RCVDIGMKKEFIL 96

VDR_XENLA STANDARD; PRT; 423 AA.
O13053;
AT 01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DE Vitamin D3 receptor (VDR) (1,25-dihydroxyvitamin D3 receptor).
VDR OR NR1I1.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;

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[1]
P SEQUENCE FROM N.A.
X MEDLINE=89071726; PubMed=2849110;
A Burnester J.K., Wiese R.J., Maeda N., Deluca H.;
T "Structure and regulation of the rat 1,25-dihydroxyvitamin D3
V receptor.";
V Proc. Natl. Acad. Sci. U.S.A. 85:9499-9502(1988).
[2]
P SEQUENCE OF 58-423 FROM N.A.
X MEDLINE=88124963; PubMed=2829212;
A Burnester J.K., Maeda N., Deluca H.F.;
T "Isolation and expression of rat 1,25-dihydroxyvitamin D3 receptor
V cDNA.";
V Proc. Natl. Acad. Sci. U.S.A. 85:1005-1009(1988).
[3]
P INTERACTION NCOA6.
X MEDLINE=20325329; PubMed=10866662;
A Mahajan M.A., Samuels H.H.;
T "A new family of nuclear receptor coregulators that integrates nuclear
V receptor signalling through CBP.";
V Mol. Cell. Biol. 20:5048-5063(2000).
P FUNCTION: Nuclear hormone receptor. VDR mediates the action of
V vitamin D3 by controlling the expression of hormone sensitive
V genes.
P SUBUNIT: Interacts with NCOA3 and NCOA6 coactivators, leading to a
V strong increase of transcription of target genes.
P SUBCELLULAR LOCATION: Nuclear.
P DOMAIN: Composed of three domains: a modulating N-terminal domain,
V a DNA-binding domain and a C-terminal steroid-binding domain.
P SIMILARITY: Belongs to the nuclear hormone receptor family. NR1
V subfamily.

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V between the Swiss Institute of Bioinformatics and the EMBL outstation
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V modified and this statement is not removed. Usage by and for commercial
V entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
V or send an email to license@isb-sib.ch).

R EMBL: J04147; AAA41089.1; .
R PIR: A31761; A31761.
R HSP: P03372; LHQ.
R TRANSFAC; T00882; .
R InterPro; IPR000536; Hormone_rec_lig.
R InterPro; IPR001723; Stdhrm_receptor.
R InterPro; IPR001628; Znf_C4steroid.
R Pfam; PF00104; hormone_rec; 1.
R Pfam; PF00105; zf-C4; 1.
R PRINTS; PRO0398; STRDHORMONER.
R PRINTS; PRO0047; STROIDFINGER.
R PRODOM; PD000035; Znf_C4steroid; 1.
R SMART; SM00430; HOL1; 1.
R SMART; SM00399; Znf_C4; 1.
R PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
R Receptor; Transcription regulation; DNA-binding; Nuclear protein;
W Zinc-finger; Phosphorylation.
W DNA_BIND 24 89 NUCLEAR RECEPTOR-TYPE.
T ZN_FING 24 44 C4-TYPE.
T ZN_FING 60 84 C4-TYPE.
T DOMAIN 90 187 HINGE.
T DOMAIN 188 423 LIGAND-BINDING.
T SEQUENCE 423 AA; 47813 MW; 1A0E519A9DCE990 CRC64;
Query Match 10.6%; Score 68.5; DB 1; Length 423;
Best Local Similarity 30.1%; Pred. No. 7.2;
Matches 22; Conservative 13; Mismatches 15; Indels 23; Gaps 6;
Y 50 CF-CKDWFLAPRRKMTVSGLPKKQPCDDHFGKGVKTKRHRHPRKPKHSHRACQFLK 108
b 41 CGCGKFFRRSMKRALFT-----CP---FNGDCRITKDNR-----REQQACR--LK 82
Y 109 QC-----QLRFSAL 117

DB 83 RCVDIGMKKEFIL 95
RESULT 15
VDR_BOVIN
ID VDR_BOVIN STANDARD: PRT; 424 AA.
AC Q28037;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vitamin D3 receptor (VDR) (1,25-dihydroxyvitamin D3 receptor).
GN VDR OR NR11.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97034797; PubMed=8880453;
RA Neibergs H.L., Bosworth B.T., Reinhardt T.A.;
RT "Nucleotide sequence of the bovine vitamin D3 receptor.";
RL J. Dairy Sci. 79:1313-1315(1996).
CC FUNCTION: Nuclear hormone receptor. VDR mediates the action of
V vitamin D3 by controlling the expression of hormone sensitive
V genes.
CC SUBUNIT: Interacts with NCOA3 and NCOA6 coactivators, leading to a
V strong increase of transcription of target genes (By similarity).
CC SUBCELLULAR LOCATION: Nuclear.
CC DOMAIN: Composed of three domains: a modulating N-terminal domain,
V a DNA-binding domain and a C-terminal steroid-binding domain.
CC SIMILARITY: Belongs to the nuclear hormone receptor family. NR1
V subfamily.

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R EMBL: U50200; AB01543.1; .
R HSP: 075469; IILG.
R InterPro; IPR000536; Hormone_rec_lig.
R InterPro; IPR001723; Stdhrm_receptor.
R InterPro; IPR001628; Znf_C4steroid.
R Pfam; PF00104; hormone_rec; 1.
R Pfam; PF00105; zf-C4; 1.
R PRINTS; PRO0398; STRDHORMONER.
R PRINTS; PRO0047; STROIDFINGER.
R PRODOM; PD000035; Znf_C4steroid; 1.
R SMART; SM00430; HOL1; 1.
R SMART; SM00399; Znf_C4; 1.
R PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
R Receptor; Transcription regulation; DNA-binding; Nuclear protein;
W Zinc-finger; Phosphorylation.
W DNA_BIND 21 86 NUCLEAR RECEPTOR-TYPE.
T ZN_FING 21 41 C4-TYPE.
T ZN_FING 57 81 C4-TYPE.
T DOMAIN 87 188 HINGE.
T DOMAIN 189 424 LIGAND-BINDING.
T SEQUENCE 424 AA; 47957 MW; E9E2426CE38CB7D CRC64;
Query Match 10.6%; Score 68.5; DB 1; Length 424;
Best Local Similarity 30.1%; Pred. No. 7.2;
Matches 22; Conservative 13; Mismatches 15; Indels 23; Gaps 6;
Y 50 CF-CKDWFLAPRRKMTVSGLPKKQPCDDHFGKGVKTKRHRHPRKPKHSHRACQFLK 108
b 41 CGCGKFFRRSMKRALFT-----CP---FNGDCRITKDNR-----RHCQACR--LK 79
DB 38 CGCGKFFRRSMKRALFT-----CP---FNGDCRITKDNR-----RHCQACR--LK 79

109 QC---OLRSFAL 117
80 RCVDIGMKKEFIL 92

Search completed: September 13, 2003, 14:44:39
Job time : 23.3333 secs

GenCore version 5.1.6
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M protein - protein search, using sw model

un on: September 13, 2003, 14:39:41 ; Search time 50.6667 Seconds
(without alignments)
606.084 Million cell updates/sec

title: US-09-786-260-1

effect score: 644

sequence: 1 MKVLISLLLLPLMLMSV.....SRACQFLKCCQLRSPALPL 119

coring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

earched: 830525 segs, 258052604 residues

otal number of hits satisfying chosen parameters: 830525

inimum DB seq length: 0

aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

atabase :

SPREMBL_23:*

1: sp-archea:*

2: sp-bacteria:*

3: sp-fungi:*

4: sp-human:*

5: sp-invertebrate:*

6: sp-mammal:*

7: sp-mhc:*

8: sp-organelle:*

9: sp-phage:*

10: sp-plant:*

11: sp-rodent:*

12: sp-virus:*

13: sp-vertebrate:*

14: sp-unclassified:*

15: sp-rvirus:*

16: sp-bacteriap:*

17: sp-archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	%	ID	Description
1	322	50.0	128	11 Q8R3U6	Q8R3U6 mus musculus
2	77.5	12.0	337	5 O62022	O62022 caenorhabdi
3	77.5	12.0	449	5 Q810M4	Q810M4 caenorhabdi
4	76.5	11.9	411	13 Q9W745	Q9W745 xenopus lae
5	72.5	11.3	752	4 Q8NAP3	Q8NAP3 homo sapien
6	71.5	11.1	108	10 O82328	O82328 arabidopsis
7	71	11.0	188	4 Q8TEV2	Q8TEV2 homo sapien
8	71	11.0	543	5 Q8WQJ1	Q8WQJ1 drosophila
9	71	11.0	3390	5 O01368	O01368 drosophila
10	71	11.0	3276	5 Q9W321	Q9W321 drosophila
11	70.5	10.9	160	10 Q9SQH1	Q9SQH1 arachis hyp
12	70.5	10.9	1290	3 Q9GUA3	Q9GUA3 neurospora
13	70	10.9	117	4 Q9BRN8	Q9BRN8 homo sapien
14	70	10.9	743	5 O97120	O97120 schistosoma
15	70	10.9	746	5 Q81NJO	Q81NJO drosophila
16	70	10.9	1095	5 Q21852	Q21852 caenorhabdi

17	70	10.9	1664	5 Q9TVQ2	Q9TVQ2 caenorhabdi
18	69.5	10.8	221	12 Q85299	Q85299 crf virus.
19	69.5	10.8	468	4 Q9UC32	Q9UC32 homo sapien
20	69.5	10.8	625	4 Q8IV29	Q8IV29 homo sapien
21	69.5	10.8	653	12 Q8JTG6	Q8JTG6 human papil
22	69	10.7	111	10 Q9FWV9	Q9FWV9 oryza sativ
23	69	10.7	200	16 Q9HVU8	Q9HVU8 pseudomonas
24	69	10.7	271	4 Q9HBS0	Q9HBS0 homo sapien
25	69	10.7	378	3 Q74213	Q74213 aspergillus
26	69	10.7	400	10 Q8LEL2	Q8LEL2 arabidopsis
27	69	10.7	413	10 Q9C8W2	Q9C8W2 arabidopsis
28	69	10.7	454	13 Q9OZE8	Q9OZE8 oncorhynch
29	69	10.7	527	10 Q9SKW4	Q9SKW4 arabidopsis
30	69	10.7	1077	4 Q8N279	Q8N279 homo sapien
31	69	10.7	1081	6 Q9BE73	Q9BE73 macaca fasc
32	68.5	10.6	381	5 Q26641	Q26641 strongyloce
33	68.5	10.6	405	13 Q9PS79	Q9PS79 xenopus. xc
34	68.5	10.6	422	11 Q922X0	Q922X0 mus musculu
35	68.5	10.6	427	6 Q95MH5	Q95MH5 saguinus oe
36	68.5	10.6	1006	16 P73012	P73012 synechocyst
37	68	10.6	189	14 Q991U7	Q991U7 uncultured
38	68	10.6	283	10 Q43508	Q43508 lycopersico
39	68	10.6	291	13 Q9IAK3	Q9IAK3 xenopus lae
40	68	10.6	539	10 Q9XHV3	Q9XHV3 cryza sativ
41	67.5	10.5	453	13 Q9PTN2	Q9PTN2 brachydanio
42	67.5	10.5	1069	5 Q9BPS2	Q9BPS2 bombyx mori
43	67	10.4	376	10 Q9LXW3	Q9LXW3 arabidopsis
44	67	10.4	454	13 Q8QGE2	Q8QGE2 salmo salar
45	67	10.4	743	12 Q83111	Q83111 mouse adeno

ALIGNMENTS

RESULT 1

Q8R3U6 PRELIMINARY: PRT; 128 AA.
AC Q8R3U6; DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Similar to hypothetical gene LOC125944.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024561; AAH24561.1; ..
SQ SEQUENCE 128 AA; 14043 MW; CCE67DA04D23D7DF CRC64;

Query Match 50.0%; Score 322; DB 11; Length 128;
Best Local Similarity 70.9%; Pred. No. 7.1e-30;
Matches 61; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Qy	1	MKVLISLLLLPLMLMSVSSLNPGVARGHRDRGQASRRLQEGGCECKDWFLLRAP 60
Db	1	MKLLASPFLLLPVLMKSVFSSPNPGVARGSHGQHLAPRWLLEGGCECKDWFLLQAP 60
Qy	61	RRKFTVSGLPKKQCPDHFKNVKK 86
Db	61	KRKATAVLGPPEKQCPDHFVKGREKK 86

RESULT 2

O62022 PRELIMINARY: PRT; 337 AA.
ID O62022; O18293;
AC O62022; O18293;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

QY	46	GGQCECKDWFLRAPRR	---KFMTVSGLPKKO---CPCDHFKGNVKKTRQRRHHRKPNKHS	100
DB	262	GGNAESNTTFLRATKRRFFKRIYTSATLPKKQNSTMDNFQKSVFFEDTAHHNPMDG	321	
QY	101	RACQOFLKQCOL	112	
DB	322	R----ILKKAPL	329	
RESULT 4				
ID	Q9W745	PRELIMINARY:	PRT;	411 AA.
AC	Q9W745;			
DT	01-NOV-1999	(TREMELrel. 12, Created)		
DT	01-NOV-1999	(TREMELrel. 12, Last sequence update)		
DT	01-MAR-2003	(TREMELrel. 23, Last annotation update)		
DE	COUP	transcription factor 1.		
OC	Xenopus	laevis (African clawed frog).		
OC	Eukaryota;	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia;	Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;		
OC	Xenopodinae;	Xenopus.		
OC	NCBI_TaxID=8355;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Langlois M.C., Vanacker J.M., Holland N.D., Escriva H., Queva C.,			
RA	Laudet V., Holland L.Z.			
RT	"Amphicou-p-TF, a nuclear orphan receptor of the lancelet Branchiostoma			
RT	floridae, is implicated in retinoic acid signaling pathways."			
RL	Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.			
CC	-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).			
CC	-1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.			
DR	EMBL; AF157558; AAD42224.1; -.			
DR	HSSP; P19793; 2NLL.			
DR	InterPro; IPR000536; Hormone_rec.lig.			
DR	InterPro; IPR001723; Stdhmn_receptor.			
DR	InterPro; IPR001628; Znf_C4steroid.			
DR	Pfam; PF001104; hormone_rec; 1.			
DR	Pfam; PF00105; zf-C4; 1.			
DR	PRINTS; PR00398; STRDHORMONER.			
DR	PRINTS; PR00047; STROIDFINGER.			
DR	PRODom; PD000035; Znf_C4steroid; 1.			
DR	SMART; SM00430; HOLI; 1.			
DR	SMART; SM00399; Znf_C4; 1.			
DR	PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.			
KW	DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;			
KW	Transcription regulation; Zinc; Zinc-finger;			
SQ	SEQUENCE 411 AA; 45467 MW; 950E285B7FC336FB CRC64;			
Query Match 11.9%; Score 76.5; DB 13; Length 411;				
Best Local Similarity 26.0%; Pred. No. 1.4;				
Matches 26; Conservative 16; Mismatches 25; Indels 33; Gaps 6				
QY	26	PGVA--RGHRDGRQARRWLQ-----	-----EGGQECE-CKDWFLRAPRRKFMVVSGL 70	
DB	53	PGAAGDKGGGSGQQQHIECVCGDKSSSKHHGQQTCEGCKSFRRSVRRN-LIYTCR 111		
QY	71	PKQCCPCDHFKGNVKKTRQRRHHRKPNKHSRACQOFLKQC	110	
DB	112	ANRNCPID-----QHRRNQCCYCR-----LKKC	134	
RESULT 5				
ID	Q8NAP3	PRELIMINARY:	PRT;	752 AA.
AC	Q8NAP3;			
DT	01-OCT-2002	(TREMELrel. 22, Created)		
DT	01-OCT-2002	(TREMELrel. 22, Last sequence update)		
DT	01-MAR-2003	(TREMELrel. 23, Last annotation update)		
DE	Hypothetical protein FLJ35036 (Fragment).			
OC	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OC	NCBI_TaxID=9606;			

```

Query Match      11.13; Score 71.5; DB 10; Length 108;
Best Local Similarity 25.94; Pred. NO. 1.3;
Matches 29; Conservative 18; Mismatches 38; Indels 27; Gaps 7;

QY      1 MKVLISLLIL-LPLMLMSVSSSLNPGVARG-----HRDRGQASRRWLQEGQGCE-- 51
DB      1 MKIIIVLIULASLLLLISSLASATISDAGSGAVAPAQSKDGPALKWC---GKCEGR 57

QY      52 CKDWFLRAPRKFTWVSLPKKPCDCDFHFGKNVKTRHQRHRRKPNKHSRAC 103
DB      56 CKE---AGMKDKRLCYGICKCKQC-----VPSTGY-----GNKHECAC 94

RESULT 7
Q8TEV2 PRELIMINARY; PRT; 188 AA.
ID Q8TEV2 AC Q8TEV2 DT 01-JUN-2002 (TRENBIrel. 21, Created)
DT 01-JUN-2002 (TRENBIrel. 21, Last sequence update)
DE 01-MAR-2003 (TRENBIrel. 23, Last annotation update)
DE Vascular endothelial growth factor B isoform VEGF-B167.
GN VEGFB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_Taxid=9606;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=96325041; PubMed=8702615;
RA Olofsson B., Pajusola K., von Euler G., Chilov D., Alitalo K.,
RA Eriksson U.;
RA "Genomic organization of the mouse and human genes for vascular
RT endothelial growth factor B (VEGF-B) and characterization of a second
RT splice isoform.";
RT J. Biol. Chem. 271:19310-19317(1996).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=98032228; PubMed=9365524;
RX Joukov V., Kaipainen A., Jeltsch M., Pajusola K., Olofsson B.,
RA Kumar V., Eriksson U., Alitalo K.;
RA "vascular endothelial growth factors VEGF-B and VEGF-C.";
RT J. Cell. Physiol. 173:211-215(1997).
RN [3]
RN SEQUENCE FROM N.A.
RA Jeltsch M., Pajusola K., Chilov D., Alitalo K.;
RA Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF481110; AAL79000.1;
DR InterPro; IPR002400; GE_cysknot.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00341; PDGF_1.
DR PRINTS; PR00438; GFCSKNOT.
DR ProDom; PD001629; PD_growth_factor; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS02278; PDGF_2; 1.
SQ SEQUENCE 188 AA; 21314 MW; F04554D5A3626095 CRC64;

Query Match      11.08; Score 71; DB 4; Length 188;
Best Local Similarity 29.7%; Pred. NO. 2.7;
Matches 22; Conservative 13; Mismatches 15; Indels 24; Gaps 6;

QY      43 LQEGQCECKDNLFRAPRKFTWS-GLPKQCPCDFHFGKNVKTRHQRHRRKPNKHSR 101
DB      116 LEESHQ-CECR-----PKKKDSAVKPDSPRLCP-----RCTQHQRPD--PR 155

QY      102 AQCFLOKCOLRSF 115
DB      156 TCR---RCRRRSF 166

RESULT 8
Q8NQJ1
```


Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobaraj C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier S., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
"The genome sequence of *Drosophila melanogaster*."
Science 287:2185-2195(2000).
[2]
SEQUENCE FROM N.A.
Celisner S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
Evans C.A., Cocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
Stapleton M., Strong R., Svirskaas R., Tector C., Tyler D.,
Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.,
"Sequencing of *Drosophila melanogaster* genome."
Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A.
Mitra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
Tupy J.I., Bergman B., Carlson J.W., Celisner S.E.,
Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.,
"Annotation of *Drosophila melanogaster* genome."
Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[4]
SEQUENCE FROM N.A.
Adams M.D., Celisner S.E., Gibbs R.A., Rubin G.M., Venter C.J.,
Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[5]
SEQUENCE FROM N.A.
FlyBase:
Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
EMBL; AE003448; AAF4516.2; -;
FlyBase; FBgn0015624; neJ.
InterPro; IPR00104; Antifreeze1.
InterPro; IPR001487; Bromodomain.
InterPro; IPR003101; KIX.
InterPro; IPR000197; TAZ_finger.
InterPro; IPR000433; Znf_ZZ.
Pfam; PF00439; bromodomain; 1.
Pfam; PF02172; KIX; 1.
Pfam; PF02135; zf-TAZ; 2.
Pfam; PF00569; Z2; 1.
PRINTS; PR00308; ANTIFREEZE1.
PRINTS; PR00503; BROMODOMAIN.
SMART; SM00291; znf_ZZ; 1.
PROSITE; PS00633; BROMODOMAIN_1; 1.
PROSITE; PS00633; BROMODOMAIN_2; 1.
PROSITE; PS0134; zf-TAZ; 2.
PROSITE; PS01357; zf_ZZ_1; 1.
DR PROSITE; PS50135; zf_ZZ_2; 1.
SQ SEQUENCE 3276 AA; 340728 MW; C9D4611ACBD3918A CRC64;
Query Match 11.0%; Score 71; DB 5; Length 3276;
Best Local Similarity 26.7%; Pred. No. 52;
Matches 23; Conservative 11; Mismatches 30; Indels 22; Gaps 3;
QY 25 NPGVARGHRDQGASRRWLQGGQCECKDWFRLAPRRKFTMTYSLGPKKQCCDHFKNV 84
DB 2390 NPGQA-----RKSIQRCISLAHACQCRDANCRLP-----SCKMKLVV 2429
QY 85 KTRHQRHHRKPNKHSRACQFLKQC 110
DB 2430 QHTNCK--RKPNGGCPICQIALC 2453
RESULT 11
Q9SQH1 PRELIMINARY; PRT; 160 AA.
AC Q9SQH1;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Allergen.
GN ARA H 7.
OS Arachis hypogaea (Peanut).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Aeschynomeneae;
OC Arachis.
OX NCBI_TaxID-3818;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Virginia; TISSUE-Seed;
RX MEDLINE-99406463; PubMed-10474031;
RA Kleber-Janke T., Cramer R., Appenzeller U., Schlaak M., Becker W.M.;
RT "Selective cloning of peanut allergens including profilin and 2S
albumins, by phage display technology";
RL Int. Arch. Allergy Immunol. 119:265-274(1999).
DR EMBL; AF091737; AAB56719.1; -;
DR InterPro; IPR003612; AAI.
DR Pfam; PF00234; trypt_alpha_amy1; 1.
DR SMART; SM00499; AAI; 1.
SQ SEQUENCE 160 AA; 18417 MW; 9F9E4CEB6808D4C CRC64;
Query Match 10.9%; Score 70.5; DB 10; Length 160;
Best Local Similarity 22.1%; Pred. No. 2.6;
Matches 33; Conservative 19; Mismatches 46; Indels 51; Gaps 6;
QY 1 MKVLISILLLLPLMLSMYSSSLNPGVARGHRDQGASRRWLQGGQCECKDWFRLAP 60
DB 1 MMVKLSILVALLGALLVVASATRWDP-----DRSGSRWDAPSRGDDQCCQRLQAN 53
QY 61 RKFTVYSGLPKQPC-DHFKGNVKKTRHQRHXP-----NKHSRAC 103
DB 54 LR-----PCEHMRVRVEQEQDEPYPSRGRSGRQGESDENQRCC 100
QY 104 Q-----QFLKQ-CQLRSFALP 118
DB 101 NELNRFQNQRCMCQALQQLQNCQFWVP 129
RESULT 12
Q96UA3 PRELIMINARY; PRT; 1290 AA.
AC Q96UA3;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Hypothetical 137.8 kDa protein.
GN B1122.060.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OX		NCBI_TaxID=6183;
RN	[1]	
RP		SEQUENCE FROM N.A.
RA		MEDLINE=99143112; PubMed=9988692;
RR		Freeburn W.J., Osman A., Niles E.G., Christen L., Loverde P.T.;
RX		*Identification of a cDNA encoding a retinoid X receptor homologue
RT		from Schistosoma mansoni. Evidence for a role in female-specific gene
RT		expression.";
J.	Biol. Chem.	274:4577-4585(1999).
CC	-!	SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC	-!	SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
CC	EMBL:	AF094759; AAD16119.1; ..
DR	HSSP:	P19793; IRYX.
DR	InterPro:	IPR000536; Hormone_rec_lig.
DR	InterPro:	IPR001723; Stdhrmn_receptor.
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DR	Pfam:	PF00105; zf-C4; 1.
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DR	ProDom:	PD000035; Znfc4steroid; 1.
DR	SMART:	SMO0430; HOLI; 1..
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DT	01-MAR-2003	(TREMBLrel. 23; Last sequence update)
DE	01-MAR-2003	(TREMBLrel. 23; Last annotation update)
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OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	
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RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,	
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RA	Brandon R.C., Rogers V.H., Blazej R.G., Champe M., Pfeiffer B.D.,	
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gaber G.L.,	
RA	Abriil J.F., Agbayani A., An H.J., Andrews-Pfankuch C., Baldwin D.,	
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RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,	

GenCore version 5.1.6
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protein - protein search, using sw model

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SUMMARIES

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3	644	100.0	119	9	US-09-989-279-165 Sequence 165, App
4	644	100.0	119	9	US-09-989-727-165 Sequence 165, App
5	644	100.0	119	10	US-09-989-731-165 Sequence 165, App
6	644	100.0	119	10	US-09-989-732-165 Sequence 165, App
7	644	100.0	119	10	US-09-931-073-165 Sequence 165, App
8	644	100.0	119	10	US-09-990-442-165 Sequence 165, App
9	644	100.0	119	10	US-09-991-163-165 Sequence 165, App
10	644	100.0	119	10	US-09-983-604-165 Sequence 165, App
11	644	100.0	119	10	US-09-990-456-165 Sequence 165, App
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13	644	100.0	119	10	US-09-992-598-165 Sequence 165, App
14	644	100.0	119	10	US-09-989-293A-165 Sequence 165, App
15	644	100.0	119	10	US-09-989-735-165 Sequence 165, App

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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19	644	100.0	119	10	US-09-990-436-165 Sequence 165, App
20	644	100.0	119	10	US-09-993-687-165 Sequence 165, App
21	644	100.0	119	11	US-09-989-734-165 Sequence 165, App
22	644	100.0	119	11	US-09-997-653-165 Sequence 165, App
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28	644	100.0	119	11	US-09-990-711-165 Sequence 165, App
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34	644	100.0	119	11	US-09-997-514-165 Sequence 165, App
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36	644	100.0	119	11	US-09-991-172-165 Sequence 165, App
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ALIGNMENTS

RESULT 1
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; Sequence 165, Application US/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Nepier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: ROY, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1063
; CURRENT APPLICATION NUMBER: US/09/989,722
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17

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PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

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309-989-723-165
Sequence 165, Application US/09989723
Patent No. US20020072092A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Geurtsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ACIDS
FILE REFERENCE: P2730P1C62
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CURRENT FILING DATE: 2001-11-19
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; PRIOR FILING DATE: 1998-07-02
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 644; DB 9; Length 119;
Best Local Similarity 100.0%; Pred. No. 2.7e-62;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps

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; Patent No. US20020072496A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PLC56
; CURRENT APPLICATION NUMBER: US/09/989,279
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1997-11-24

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PRIOR FILING DATE: 1998-06-22	PRIOR APPLICATION NUMBER: 60/090252
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PRIOR FILING DATE: 1998-06-22	PRIOR APPLICATION NUMBER: 60/090349
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PRIOR FILING DATE: 1998-06-24	PRIOR APPLICATION NUMBER: 60/090444
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PRIOR FILING DATE: 1998-06-24	PRIOR APPLICATION NUMBER: 60/090676
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PRIOR FILING DATE: 1998-06-25	PRIOR APPLICATION NUMBER: 60/090694
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PRIOR FILING DATE: 1998-06-25	PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26	PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26	PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01	PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02	PRIOR APPLICATION NUMBER: 60/091544
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PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 644; DB 9; Length 119;
Best Local Similarity 100.0%; Pred No. 2,7e-62;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVLSLLLLPMLMSVSSSLNPGVARGHRDRGQASRRWLQSGGQCECKDWFLRAP 60
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61 RRKFTVSGLPKKQCPDHFKNVKKTRHQRHKKPKNSRACQOFLKQCQLRSFALPL 119
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|||||

SEQUENT 4
Sequence 165, Application US/09989727
Patent No. US20020072497A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gieritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same

FILE REFERENCE: P2730P1C65

CURRENT APPLICATION NUMBER: US/09/989,727

PRIOR FILING DATE: 2001-11-19

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945

PRIOR FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-06-17

PRIOR APPLICATION NUMBER: 60/083322

PRIOR FILING DATE: 1998-04-28

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PRIOR FILING DATE: 1998-07-02
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PRIOR FILING DATE: 1998-07-02
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
Query Match 100.0%; Score 644; DB 9; Length 119;
Best Local Similarity 100.0%; Pred. No. 2.7e-62;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKVLISLLILLPLMLSMVSSSLNPGVARGHRRDRGQASRRWLQEGGQCECKDWFLRAP 60
DB 1 MKVLISLLILLPLMLSMVSSSLNPGVARGHRRDRGQASRRWLQEGGQCECKDWFLRAP 60
QY 61 RRKFTVSGLPKQPCDHFKNVKKTRHORHRRKPNKHSRACQQLKQCQLRSFALPL 119
DB 61 RRKFTVSGLPKQPCDHFKNVKKTRHORHRRKPNKHSRACQQLKQCQLRSFALPL 119

RESULT 5

US-09-989-731-165
; Sequence 165, Application US/09989731
; Patent No. US20020103125A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC70
; CURRENT APPLICATION NUMBER: US/09/989,731
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/065770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28

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PRIOR FILING DATE: 1998-06-26	PRIOR APPLICATION NUMBER: 60/090663
PRIOR FILING DATE: 1998-06-26	PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01	PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02	PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01	PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02	PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02	PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02	PRIOR APPLICATION NUMBER: 60/091633

PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.08; Score 644; DB 10; Length 119;
Best Local Similarity 100.08; Pred. No. 2.7e-62;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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b 1 MKVLISLLLLPLMLSMVSSSLNPGVARGHRDRGQASRRWLQEGGQCECKDWFRLAP 60
|||||

y 61 RKFTVSVGLPKQPCDHFKNVYKTRHQHHKPKNKHRSRACQFLKQCLRSFALPL 119
|||||
b 61 RKFTVSVGLPKQPCDHFKNVYKTRHQHHKPKNKHRSRACQFLKQCLRSFALPL 119
|||||

ESULT 6
S-09-989-732-165
Sequence 165, Application US/09989732
Patent No. US20020123463A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavich, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC57
CURRENT APPLICATION NUMBER: US/09/989,732
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR FILING DATE: 1997-11-12
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PRIOR FILING DATE: 1997-11-24
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 644; DB 10; Length 119;
Best Local Similarity 100.0%; Pred. No. 2.7e-62;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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Db 1 MKVLLSSLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGCECKQDFLRAP 60
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Db 61 RRKFTVSVGLPKKQPCDHFHKGNVKTKTRQHRHRKPNKHSRACQFLKQCQLRSFALPL 119

RESULT 7
US-09-991-073-165
; Sequence 165, Application US/09991073
; Patent No. US20020127576A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul, J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC15
; CURRENT APPLICATION NUMBER: US/09/991,073
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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 PRIORITY FILING DATE: 1998-06-18
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Query Match 100.0%; Score 644; DB 10; Length 119;
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SULT 8

-09-990-442-165
 Sequence 165, Application US/09990442
 Patent No. US20020132252A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
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 APPLICANT: Godowski, Paul J.
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 APPLICANT: Kijavini, Ivar J.
 APPLICANT: Napier, Mary A.
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 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: P2730P1C8
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PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 644; DB 10; Length 119;
Best Local Similarity 100.0%; Pred. No. 2.7e-62;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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SULT 10
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Sequence 165, Application US/09993604
Patent No. US20020137075A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
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APPLICANT: Gurney, Austin L.
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APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PLC25
CURRENT APPLICATION NUMBER: US/09/993,604
CURRENT FILING DATE: 2001-11-14
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PRIOR FILING DATE: 1998-07-07
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 644; DB 10; Length 119;
Best Local Similarity 100.0%; Pred. No. 2.7e-62;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1 MKVLISLLLLPLMLMSVSSLPVARGHRDRGQASRRRLQGGQCECKDWFLRAP 60
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QY 61 RRKFMVTVSGLPKKQPCDHFHKGKGNVKKTRHRRHRRKPNKHSRACQOFLKQCOLRSFALPL 119
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DB 61 RRKFMVTVSGLPKKQPCDHFHKGKGNVKKTRHRRHRRKPNKHSRACQOFLKQCOLRSFALPL 119
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RESULT 11
US-09-990-456-165
; Sequence 165, Application US/09990456
; Patent No. US20020137890A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC22
; CURRENT APPLICATION NUMBER: US/09/990,456
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 644; DB 10; Length 119;
Best Local Similarity 100.0%; Pred. No. 2.7e-62;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGQCECKDFLRAP 60
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S-09-989-721-165

Sequence 165, Application US/09989721

Patent No. US20020142961A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kijavind, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

ACIDS Encoding the Same

FILE OF INVENTION: P27301C55

CURRENT APPLICATION NUMBER: US/09/989,721

CURRENT FILING DATE: 2001-11-19

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PRIOR FILING DATE: 1997-06-16

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PRIOR FILING DATE: 1998-07-07
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PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 644; DB 10; Length 119;
Best Local Similarity 100.0%; Pred. No. 2.7e-62;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 1 MKVLISLLLLPLMLSMVSSSLNPGVARGHRDRGQASRRWLQGGQCECKDWFRLAP 60
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Y 61 RRKFWTVSLPKKQPCDFKGNVKKTRHQRHHRKPNKHSRACQFLKQCOLRGSFALPL 119
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RESULT 13

US-09-992-598-165
Sequence 165, Application US/09992598
Patent No. US20020160384A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
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APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P.C20
CURRENT APPLICATION NUMBER: US/09/992,598
CURRENT FILING DATE: 2001-11-14
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PRIOR FILING DATE: 1998-07-07
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 644; DB 10; Length 119;

Best Local Similarity 100.0%; Pred. No. 2,7e-62;

Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGQCECKDWFRLAP 60

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RESULT 14

US-09-989-293A-165

; Sequence 165, Application US/0989293A

; Patent No. US20020177154A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC66
CURRENT APPLICATION NUMBER: US/09/989,293A
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/043787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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 Prior Application Number: 60/091978
 Prior Filing Date: 1998-07-07
 Prior Application Number: 60/091982
 Prior Filing Date: 1998-07-07
 Prior Application Number: 60/092182
 Prior Filing Date: 1998-07-09

Query Match 100.0% Score 644; DB 10; Length 119;
 Best Local Similarity 100.0%; Pred. No. 2.7e-62;
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 S-09-989-735-165
 Sequence 165, Application US/09989735
 Publication No. US20020193299A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kljavin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas P.
 APPLICANT: ROY, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2730P1C61
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PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 644; DB 10; Length 119;
Best Local Similarity 100.0%; Pred. No. 2.7e-62;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKVLISLLILLPLMLMSVSSSLNPGVARGHRRDQASRRWLQEGQCECKDWFRLAP 60
DB 1 MKVLISLLILLPLMLMSVSSSLNPGVARGHRRDQASRRWLQEGQCECKDWFRLAP 60
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Search completed: September 13, 2003, 14:48:18
Job time : 23 secs

GenCore version 5.1.6
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1 protein - protein search, using sw model

in on: September 13, 2003, 14:41:13 ; Search time 18 seconds
(without alignments)
279,722 Million cell updates/sec

File: US-09-786-260-1

Search score: 644

Sequence: 1 MKVLISLLLLPLMLSMV.....SRACQFLKQCLRSFALPL 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Aligned: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents.AA.*

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- 2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	644	100.0	119	4	US-09-996-243-165
2	84.5	13.1	620	4	US-09-252-991A-17301
3	74	11.5	629	4	US-09-252-991A-16777
4	73.5	11.4	70	1	US-07-737-736B-3
5	72.5	11.3	724	4	US-09-252-991A-28517
6	72	11.2	689	4	US-09-252-991A-19258
7	70.5	10.9	420	4	US-09-252-991A-27610
8	70	10.9	188	1	US-08-469-427A-11
9	70	10.9	188	2	US-08-609-443B-11
10	70	10.9	188	2	US-08-569-053C-11
11	70	10.9	188	3	US-08-795-430-57
12	70	10.9	188	4	US-08-851-896-11
13	70	10.9	188	4	US-09-355-700-57
14	70	10.9	188	4	US-09-431-888-6
15	70	10.9	626	4	US-09-252-991A-30510
16	69.5	10.8	446	1	US-08-307-444A-5
17	69.5	10.8	446	1	US-08-587-389-5
18	69.5	10.8	456	1	US-08-307-444A-3
19	69.5	10.8	456	1	US-08-307-444A-4
20	69.5	10.8	456	1	US-08-587-389-3
21	69.5	10.8	456	1	US-08-587-389-4
22	69.5	10.8	475	1	US-08-307-444A-1
23	69.5	10.8	475	1	US-08-307-444A-2
24	69.5	10.8	475	1	US-08-587-389-1
25	69.5	10.8	475	1	US-08-587-389-2
26	69.5	10.8	476	1	US-08-014-723-1
27	69.5	10.8	476	1	US-08-014-723-2

28	69.5	10.8	476	1	US-08-014-723-18
29	69.5	10.8	476	1	US-08-110-011A-1
30	69.5	10.8	476	1	US-08-110-011A-2
31	69.5	10.8	476	1	US-08-110-011A-18
32	69.5	10.8	494	1	US-08-014-723-14
33	69.5	10.8	494	1	US-08-014-723-16
34	69.5	10.8	494	1	US-08-110-011A-14
35	69.5	10.8	494	1	US-08-110-011A-16
36	69.5	10.8	497	1	US-08-312-870-3
37	69.5	10.8	497	4	US-09-331-793-4
38	69.5	10.8	498	2	US-08-733-564-2
39	69.5	10.8	568	4	US-09-252-991A-27039
40	69.5	10.8	575	1	US-08-361-206A-59
41	69.5	10.8	575	1	US-08-312-870-1
42	69.5	10.8	575	1	US-08-170-290A-54
43	69.5	10.8	575	6	5466668-6
44	69	10.7	229	4	US-09-252-991A-21486
45	69	10.7	261	4	US-09-252-991A-21486

ALIGNMENTS

RESULT 1
US-09-996-243-165
; Sequence 165, Application US/09996243
; Patent No. 6478253

- GENERAL INFORMATION:
- APPLICANT: Ashkenazi, Avi J.
- APPLICANT: Baker, Kevin P.
- APPLICANT: Botstein, David
- APPLICANT: Desnoyers, Luc
- APPLICANT: Eaton, Dan L.
- APPLICANT: Ferrara, Napoleone
- APPLICANT: Fong, Sherman
- APPLICANT: Gerber, Hanspeter
- APPLICANT: Gerritsen, Mary E.
- APPLICANT: Goddard, Audrey
- APPLICANT: Godowski, Paul J.
- APPLICANT: Grimaldi, J. Christopher
- APPLICANT: Gurney, Austin L.
- APPLICANT: Kljavin, Ivar J.
- APPLICANT: Napier, Mary A.
- APPLICANT: Pan, James
- APPLICANT: Paoni, Nicholas F.
- APPLICANT: Roy, Margaret Ann
- APPLICANT: Stewart, Timothy A.
- APPLICANT: Tumas, Daniel
- APPLICANT: Watanabe, Colin K.
- APPLICANT: Williams, P. Mickey
- APPLICANT: Wood, William I.
- APPLICANT: Zhang, Zemin
- TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same
- FILE REFERENCE: P2730P1C13
- CURRENT APPLICATION NUMBER: US/09/996,243
- CURRENT FILING DATE: 2001-11-14
- PRIOR APPLICATION NUMBER: 60/043787
- PRIOR FILING DATE: 1997-06-16
- PRIOR APPLICATION NUMBER: 60/062250
- PRIOR FILING DATE: 1997-10-17
- PRIOR APPLICATION NUMBER: 60/065186
- PRIOR FILING DATE: 1997-11-12
- PRIOR APPLICATION NUMBER: 60/065311
- PRIOR FILING DATE: 1997-11-13
- PRIOR APPLICATION NUMBER: 60/065770
- PRIOR FILING DATE: 1997-11-24
- PRIOR APPLICATION NUMBER: 60/075945
- PRIOR FILING DATE: 1998-02-25
- PRIOR APPLICATION NUMBER: 60/078910
- PRIOR FILING DATE: 1998-03-20
- PRIOR APPLICATION NUMBER: 60/083322
- PRIOR FILING DATE: 1998-04-28

PRIOR FILING DATE: 1998-06-17	PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17	PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17	PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18	PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18	PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18	PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19	PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19	PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19	PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22	PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22	PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22	PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23	PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23	PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24	PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24	PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24	PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24	PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24	PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24	PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24	PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24	PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24	PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24	PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25	PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25	PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25	PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25	PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25	PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25	PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26	PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26	PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01	PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02	PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01	PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02	PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02	PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02	PRIOR APPLICATION NUMBER: 60/091633

PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 644; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 4; le-59; Indels 0; Gaps 0;
Matches 119; Conservative 0; Mismatches 0;

1 MKVLSLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQGGQCECKDWFLRAP 60

1 MKVLSLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQGGQCECKDWFLRAP 60

61 RRKFMVSGLPKQCPDHFKNVKTQRHHRKPNKHSRACQFLKQCOLRSFALPL 119

61 RRKFMVSGLPKQCPDHFKNVKTQRHHRKPNKHSRACQFLKQCOLRSFALPL 119

SULT 2

-09-252-991A-17301
Sequence 17301, Application US/09252991A
Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 17301

LENGTH: 620

TYPE: PRT
ORGANISM: Pseudomonas aeruginosa

-09-252-991A-17301

Query Match 13.1%; Score 84.5; DB 4; Length 620;
Best Local Similarity 30.7%; Pred. No. 0.099;
Matches 27; Conservative 11; Mismatches 23; Indels 27; Gaps 4;

29 ARGHRDRGQA-----SRWLQGGQCECKDWFLRAPRRKFMVSGLPKQCPDHFKN 83

538 ARSHDRGQQRDNHRRHRRHREGRGQRE--DOYRREPHR-----GR 576

84 VKTRHQRHHRKPNKHSRACQFLKQCO 111

577 RQQRDHQ-HRRRPHREGRGQQRQDHRQC 603

SULT 3

-09-252-991A-16777
Sequence 16777, Application US/09252991A
Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 16777

LENGTH: 629

TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16777

Query Match 11.5%; Score 74; DB 4; Length 629;
Best Local Similarity 30.2%; Pred. No. 1.8;
Matches 32; Conservative 10; Mismatches 28; Indels 36; Gaps 7;

QY 24 LNPGV-----ARGHRDRGQASRR-----WLQGGQCECKDWFLRAPRRKFMVSGLPK 72

Db 448 VFPGLDDLRLRRLRHQRGRHRLRLRQLWLFQGG-----RDERR---SVARLFR 494

QY 73 KQCPDHFKNVKTQRHHRKPNKHSRACQFLKQCOLRSFALP 118

Db 495 -----HLHG-----VHRLHRSRDRH-RGAPALEQPARRTGKP 528

RESULT 4

US-07-737-736B-3
Sequence 3, Application US/07737736B
Patent No. 5260199

GENERAL INFORMATION:

APPLICANT: Deluca, Hector F.

APPLICANT: Ross, Troy K.

APPLICANT: Prahl, Jean M.

TITLE OF INVENTION: Method Of Producing

TITLE OF INVENTION: 1,25-Dihydroxyvitamin D3 Receptor Protein

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Carl R. Schwartz, Esq., c/o Quarles & Brady

STREET: 411 East Wisconsin Avenue

CITY: Milwaukee

STATE: Wisconsin

COUNTRY: U.S.A.

ZIP: 53202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/737,736B

FILING DATE: 19910730

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Schwartz, Carl R.

REGISTRATION NUMBER: 29,437

REFERENCE/DOCKET NUMBER: 96-296-2185-2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 414-277-5715

TELEFAX: 414-277-5774

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 70 amino acids

TYPE: AMINO ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Chicken

PUBLICATION INFORMATION:

AUTHORS: McDonnell, Donald P.

AUTHORS: Mangelsdorf, David J.

AUTHORS: Pike, J. W.

AUTHORS: Haussler, Mark R.

AUTHORS: O'Malley, Bert W.

TITLE: Molecular Cloning of Complementary DNA

TITLE: Encoding the Avian Receptor for Vitamin D

JOURNAL: Science

VOLUME: 235

PAGES: 1214-1217

FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 41979CP2
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
TISSUE TYPE: human fibrosarcoma
-08-469-427A-11

Query Match 10.9%; Score 70; DB 1; Length 188;
Best Local Similarity 28.4%; Pred. No. 1.2;
Matches 21; Conservative 12; Mismatches 17; Indels 24; Gaps 5;

43 LOEGGQCECKDWFLRAPRRKMTVS-GLPKKQCPDHFHKGNNKTRHQRHRRKPKNHSR 101
116 LEHSQ-CECR-----PKKDSAVKPDSPRLCP-----RCTQHQRDPDPTC 157
102 ACQOFLKQCOLRSF 115
158 RC-----RCRRRSF 166

SUIT 9
-08-609-443B-11
Sequence 11, Application US/08609443B
Patent No. 5840693
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: OLOFSSON, Birgitta
APPLICANT: ALITALO, Kari
APPLICANT: PAJUSOLA, Katri
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,443B
FILING DATE: 01-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
PRIOR APPLICATION NUMBER: US 08/469,427
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569,063

FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/41979CP4
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
TISSUE TYPE: human fibrosarcoma
US-08-609-443B-11

Query Match 10.9%; Score 70; DB 2; Length 188;
Best Local Similarity 28.4%; Pred. No. 1.2;
Matches 21; Conservative 12; Mismatches 17; Indels 24; Gaps 5;

43 LOEGGQCECKDWFLRAPRRKMTVS-GLPKKQCPDHFHKGNNKTRHQRHRRKPKNHSR 101
116 LEHSQ-CECR-----PKKDSAVKPDSPRLCP-----RCTQHQRDPDPTC 157
102 ACQOFLKQCOLRSF 115
158 RC-----RCRRRSF 166

RESULT 10
US-08-569-063C-11
Sequence 11, Application US/08569063C
Patent No. 5928939
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: OLOFSSON, Birgitta
APPLICANT: ALITALO, Kari
APPLICANT: PAJUSOLA, Katri
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,063C
FILING DATE: 06-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/469,427
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/41979CP3
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 188 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ORIGINAL SOURCE: human fibrosarcoma

TISSUE TYPE:

US-569-063C-11

Query Match

Best Local Similarity 10.9%; Score 70; DB 2; Length 188;

Matches 21; Conservative 12; Mismatches 17; Indels 24; Gaps 5;

43 LOEGGCECECKDFLRAPRRKFMVVS-GLPKKQCPDHFKNVYKTRHORHHRKPNKHRSR 101

116 LEEHSQ-CECR-----PKKDSAVKPSRPLCP-----RCTQHQRDPPTC 157

102 ACQQLKQCLRSF 115

158 RC-----RCRRSF 166

SULT 11

-08-795-430-57

Sequence 57, Application US/08795430

Patent No. 6130071

GENERAL INFORMATION:

APPLICANT: Altalo, Kari

APPLICANT: Joukov, Vladimir

TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)

TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/795,430

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/FR96/00427

FILING DATE: 01-AUG-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/671,573

FILING DATE: 28-JUN-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/601,132

FILING DATE: 14-FEB-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/585,895

FILING DATE: 12-JAN-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/510,133

FILING DATE: 01-AUG-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/340,011

FILING DATE: 14-NOV-1994

ATTORNEY/AGENT INFORMATION:

NAME: Gass, David A.

REGISTRATION NUMBER: 38,153

REFERENCE/DOCKET NUMBER: 28967/33691

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 57:

SEQUENCE CHARACTERISTICS:

LENGTH: 188 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-795-430-57

Query Match

Best Local Similarity 10.9%; Score 70; DB 3; Length 188;

Matches 21; Conservative 12; Mismatches 17; Indels 24; Gaps 5;

QY 43 LOEGGCECECKDFLRAPRRKFMVVS-GLPKKQCPDHFKNVYKTRHORHHRKPNKHRSR 101

Db 116 LEEHSQ-CECR-----PKKDSAVKPSRPLCP-----RCTQHQRDPPTC 157

QY 102 ACQQLKQCLRSF 115

Db 158 RC-----RCRRSF 166

RESULT 12

US-08-851-896-11

Sequence 11, Application US/08851896

Patent No. 6331301

GENERAL INFORMATION:

APPLICANT: ERIKSSON, Ulf

APPLICANT: OLOFSSON, Birgitta

APPLICANT: ALITALO, Kari

APPLICANT: PAJUSOLA, Katri

TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND

TITLE OF INVENTION: DNA CODING THEREFOR

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.

STREET: 1200 G Street, N.W., Suite 700

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/851,896

FILING DATE: 06-MAY-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/609,443B

FILING DATE: 01-MAR-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/397,651

FILING DATE: 01-MAR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/469,427

FILING DATE: 06-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/569,063

FILING DATE: 06-DEC-1995

ATTORNEY/AGENT INFORMATION:

NAME: EVANS, Joseph D

REGISTRATION NUMBER: 26,269

REFERENCE/DOCKET NUMBER: 1064/41979CP4

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 628-8800

TELEFAX: (202) 628-8844

INFORMATION FOR SEQ ID NO: 11:

